STIC-Biotech/ChemLib

69910

Fr m: Sent: To: Subject: Nguyen, Quang (AU1632) Monday, June 03, 2002 3:14 PM STIC-Biotech/ChemLib Sequence search request for 09/721543

Good afternoon,

Please search:

SEQ ID NO:12, 13, 14, 15 and 16 against commercial, issued and pending U.S. application databases. Should there be questions, please contact me at 308-8339 (CM1-12A12, AU 1636, my mail box is in CM1-11E12).

THANK YOU.

RECEIVED 201

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher:	TYPE OF SEARCH: NA Sequences:	VENDOR/COST(where applic.) STN:
Phone:	AA Sequences:	DIALOG:
Location:	Structures:	Questel/Orbit:
Date Picked Up:	Bibliographic:	DRLink:
Date Completed: 6-5-02	Litigation:	Lexis/Nexis:
Searcher Prep/Review:	Full text:	Sequence Sys.:
Clerical:	Patent Family:	WWW/Internet:
Online time:	Other:	Other (specify):

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OM nucleic - nucleic search, using sw model

June 4, 2002, 17:09:09; Search time 4272.65 Seconds (without alignments) 116.880 Million cell updates/sec Run on:

US-09-721-543A-16 37

1 ctatatccacccatatccccttccccttgcgtggg 37 Perfect score:

Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

13736207 seqs, 6748477542 residues Searched:

27472414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

gb_gss:*
em_gss_hum:*
em_gss_inv:*
em_gss_lns:* em_estba:*
em_esthum:*
em_estin:*
em_estin:*
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em_estip:*
em_estip:*
em_estip:*
em_estip:*
gb_esti:*
gb_esti:* EST: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_vrt:*

A2908796 RPCI-24-1 A2342846 RPCI-24-1 A2343364 RPCII-13 B1682748 463908 MA A1381292 ct-64564.x AW531399 UI-R-BSO-BF416687 UI-R-BSO-AW43371 UI-R-BO-AW453771 UI-R-BO-AW55658 AV656658 A997381 UI-R-CO-h BG381507 UI-R-CIO-A3752617 AV752617 RE965557 G01528842 BE911323 601658842 BE911323 601652233 BF688465 602185067 Description SUMMARIES A2908796 A274846 A2748364 B1682748 A0746618 A0746618 AA31199 BF415687 AW331199 BF415687 AW33771 AV56558 AA997381 AV55617 BE911323 BF9689655 BF9689655 010 066 1000 Query Match Length DB 564 934 359 1197 1197 306 306 340 478 504 696 696 696 696 696 6662. 666111. 666111. 666111. 66611. Score Result 8 0000 00000000000

AW242494 xm99f06.x BF226236 uz48c10.y A1151930 ui47h06.y BF286029 EST450620	(μ)	m 01 01	BH408135 1007056D0 BF039832 BP250015A BM365942 BS3200200 AW657071 109692 MA BH631145 1007074C0 BI540444 453734 MA	Æ
AW242494 BF226236 AII51930 BF286029 BF990118	BB140912 BG923513 BG620158 B1688856 B1645932	B1522467 BH626108 AW353241 AW356268 BH628904 AW478514 BE753768 BH625558	BH408135 BH303932 BM365942 AW657071 BH631145 BI540444	AG054991 AZ274408 AI328516 BI490098
90000	169999	120919919	229622	122
288 376 523 544 600	683 698 762 764 815	822 2122 265 348 379 442 475	475 519 543 574	1350 413 420 480
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21.6 21.6 21.6 21.6 21.6	21.6 21.6 21.6 21.6 21.6	2211.6	21.2 21.2 21.4 21.4 4.4.4 4.4.4	21.2 21.2 21.2 21.2
c 18 c 19 22 22	00000 00000 00000	~~~~~~~	C 36 337 C 40 41	000 4444 8848, '

ALIGNMENTS

A2908796 513 bp DNA linear GSS 05-WAR-2001 RPCI-24-222E16.TJ RPCI-24 Mus musculus genomic clone RPCI-24-222E16 A2908796 A2908796.1 GI:13227741	house mouse. Mus musculus. Mus musculus. Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 513) Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvatsbeyn,R., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.	Mouse BAC End Sequences from Library RPCI-24 Unpublished (1999) Contact: Shaying Zhao Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA TTel: 301 838 0200 Fax: 301 838 0200 Email: szhaodétigr.org Elones are derived from the mouse BAC library RPCI-24. For BAC Clones are derived from the mouse contact Pieter de Jong	(pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.chori.org/bacpac/orderingframe.htm). BAC end plate: 222 row: E column: 16 Seq primer: SP6 Class: BAC ends. Location/Qualifiers: Location/Qualifiers: Location/Qualifiers: //stain="CSDBL/60" //db_xref="taxon:10090" //clone="RPCI-24"
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RPCII1-137E20.TV RPCI-11 Homo sapiens genomic clone RPCI-11-137E20,
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
1 162 c 130 g 144 t 2 others
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   Mismatches
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/db_xref="CDB:752339"
/db_xref="taxon:9606"
/clone="RPCI-11-137E20"
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/organism="Homo sapiens"
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24; Conservative
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               /cell_type="Spleen/Brain"
/hote="Vector: pTARBACL; Site_1: BamH1; Site_2: BamH1;
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/RPCT-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBACL cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
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Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
Tel: 301 838 0208
Fax: 301 838 0208
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/clone="RPCT-24-110L21"
/clone="Lib="RPCT-24"
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/RPCT-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using Mbol partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Bate: ill row: L column: 21
Class: BAC ends.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 278)
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                                                                                                                                                                                                                                                                                                                           Score 23; DB 12; Length 513;
Pred. No. 3.9e+02;
0; Mismatches 5; Indels
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/organism="Mus musculus"
/strain="C57BL/6J"
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AZ742846
AZ742846.1 GI:12522124
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83.9%;
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92.3%;
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Matches 26; Conserv
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Best Local Similarity
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RESULT 2 A2742846/c

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

BASE COUNT ORIGIN

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Gaps

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EST 17-SEP-2001

BASE COUNT

FEATURES

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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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AQ746618.1 GI:5533776
                                                              1 (bases 1 to 564)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
,G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Keele, J.W.
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                            Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahalras GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tal: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 CTTCCTCCATCCACATCCCCTTGCCATCCGTGAGGG 325
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/clone_lib="MARC 1BOV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACKWARD: GTTTTCCCAGTCACGACG
Plate: 133 row: E column: 23
Seq primer: ATTTAGGTGACACTATAG.
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Matches 28; Conserv
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (infoëlmage.llnl.gov) for further information.
Insert Length: 851 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 324.
Location/Qualifiers
1. 359
/organism-Homo sapiens"
/doxanism-Homo sapiens"
/doxanism-Homo sapiens"
/clone="IMAGE:2067967"
/clone="IMAGE:2067967"
/lab host="Rullo"Soares_total_fetus_Nb2HF8_9w"
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401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3618 Eax: (206) 616-3618 Eax: (206) 616-3618 Eaxi (206) 616
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 359)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="Plate=2278 Col=10 Row=M"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI381292 359 bp mRNA linear EST 18-MAR-1 tc49f04.xl Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2067967 3' similar to gb:x56667_rnal CALRETININ (HUMAN);,
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 6.1e+02;
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/db_xref="taxon:9606"
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Location/Qualifiers
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A1381292.1 GI:4194073
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75.7%;
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us-09-721-543a-16.rst

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Length 197;

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Ouery Match 58.9°
Best Local Similarity 78.8°
Matches 26; Conservative
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/strain="Sprague-Dawley"
/db_ref="Laxon:10116"
/db_ref="Laxon:10116"
/clone="UI-R-BSO-amm-e-05-0-UI"
/clone="UI-R-BSO-amm-e-05-0-UI"
/clone="UI-R-BSO"
/dey_stage="embryonic 13 dpc"
/dab_host="mblyonic 13 dpc"
/dab_host="DH108 (Life Technologies)"
/lab_host="DH108 (Life Technologies)"
/note="Vector: pT773D-psc (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BSO
library is derived from 13 dpc whole embryo tissue. For a
detailed description of the library from which this clone
was derived, please visit our web site at
referst.eng.ulowa.edu.
                                                                                                                                                                                                                                                                                                                                                                 AW531399 197 bp mRNA linear EST 06-MAR-2000 UI-R-BSO-amm-e-05-0-UI.sl UI-R-BSO Rattus norvegicus cDNA clone UI-R-BSO-amm-e-05-0-UI 3', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
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Fax: 319 335 9565
                                                                                                                                                                           Gaps
one round of normalization, and was by Bento Soares and M. Fatima Bonaldo. 108 g \, 67 t \, 2 others
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                                                                                                                                 Length 359;
                                                                                                         Score 22; DB 9; Length 323
Pred. No. 7.9e+02;
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Program for Rat Gene Discovery and Mapping
University of Iowa
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97044477
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went through constructed bases 80 c
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                                                                                                                               59.5%;
78.1%;
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Matches 25; Conservative
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Wilvering Medical Research Building Iowa City, IA 52242, USA Tel: 319 315 8250
Fax: 319 315 8250
Fax: 319 315 8250
Fax: 319 315 8250
Email: msoarce@blue.weeg.ulowa.edu
The sequence contained an oligo-dT track that was present in the oligounclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonsfide poly A tail. The sequence tag present in the CDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized fundus library cDNA Library Preparation: M.B. Soarcs Lab Genetics (www.resgen.com) The following repetitive elements were found in this CDNA sequence: 1-21, >AT_rich#Low_complexity
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//dev_
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
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58.9%; Score 21.8; DB 9; 78.8%; Pred. No. 8.1e+02; ive 0; Mismatches 7;
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/clone="UT-R-CNO-bkz-b-11-0-UI"
/clone=1lb-"UI-R-CNO"

    .281
    /organism="Rattus norvegicus"

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97044477
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TAG_LIB-UI-R-CN0
TAG_TISSUE-fundus
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Homo sapiens

Eukaryota; Metazoa; Chordatu; Cranlata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

It (bases 1 to 369)

Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,

Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,

Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,

Hu,G., Gu,J., Chen,Z. and Han,Z.

Insight into hepatocellular carcinogenesis at transcriptome level

by comparing gene expression profiles of hepatocellular carcinoma

with those of corresponding noncancerous liver

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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                                                                                                                                                                                                                                                                              AV656658 369 bp mRNA linear EST 16-JAN-2002
AV656658 GLC Homo sapiens cDNA clone GLCETF05 3', mRNA sequence.
AV656658.1 GI:9877672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="corresponding non cancerous liver tissue" /dev_stage="Adult" /lab host="Solls" /lab host="Solls" /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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                            No. 9e+02;
                          Pred. No. 9e+(
0; Mismatches
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/db_xref="taxon:96(6"
/clone="GLCETF05"
/clone_lib="GLC"
                                                                                                   1 ctatatccacccatatccccttccccttgcgtg
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Best Local Similarity 78.8
Matches 26; Conservative
                                                 Conservative
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                          Best Local Similarity
Matches 26; Conserv
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AA997381/c
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761: 319 335 8250

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Fax: 319 335 9565

Fax: 319 336 9660

Fax: 319 36 9660

Fax: 310 9660

Fax
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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. 8.8e+02;
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/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="Ur_R-BMOP-afq-g-08-0-UI"
/clone_1lb="UI-R-BMOP"
/dev_stage="adult"
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Program for Rat Gene Discovery and Mapping
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TAG_LIB=UI-R-BJOp
TAG_TISSUE=AV canal at 16.5 dpc
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                       Pred. No. 8.86
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                    Best Local Similarity 78.8%;
Matches 26; Conservative
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Gaps

EST 12-MAR-2001

REFERENCE AUTHORS

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MEDLINE COMMENT JOURNAL

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Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: msoares@blue.weeg.ulowa.edu

The sequence contained an oligo-dT track that was present in the oligonerlectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Noti site and the oligo-dT track served to verify it as a clone from the normalized rat brain pool library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                 Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
BG381507
UI-R-CTJ-buk-b-05-0-UI.sl UI-R-CTO Rattus norvegicus CDNA clone
UI-R-CTJ-buk-b-05-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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Rattus norvegicus
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//deb_host="DH10B (Life Technologies)"
//deb_host="DH10B (Life Technologies)"
//deb_host="DH10B (Life Technologies)"
//deb_wetor: pT773D-pac (Pharmacia) with a modified
polyllnker; Site_1: Not I; Site_2: Eco RI: The UI-R-CO
library is a subtracted library derived from the UI-R-CO
library is a subtracted library derived from the UI-R-G
and UI-R-EI libraries. The UI-R-AI library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, and muscle. The UI-R-EI
library consisted of a mixture of individually tagged
normalized libraries constructed from 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dr track which
allows identification of the library of origin of a clone
within the mixture. The subtracted library (UI-R-CO) was
constructed as follows: PCR amplified cDNA inserts from a
pool of UI-R-AI and UI-R-EI clones from which 3' ESTS had
been derived was used as a diriver in a hybriolization with
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the CDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized adult 12-Day-Embryo library. CDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through the I.M.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the pooled UT-R-Al and UT-R-EI library in the form of single-stranded circles. The remaining single-stranded circles. The remaining single-stranded circles and proxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UT-R-CO library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                           1 (bases 1 to 370)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                               University of Iowa 451 Ecsearch Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                          On Jun 5, 1998 this sequence version replaced gi:3188164
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.9%; Score 21.8; DB 9; Length 370; 78.8%; Pred. No. 9.4e+02; ive 0; Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="U1-R-C0"
/dev_stage="adult"
                                                                                                                                                        Genome Res. 6 (9), 791-806 (1996)
97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Best Local Similarity
Matches 26; Conserv
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                                                                                                                                       discovery
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source

FEATURES

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EST 05-APR-1999
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                                                                                                           Length 478;
                                                                                                                                       Indels
                                                                                                       58.9%; Score 21.8; DB 10; 78.8%; Pred. No. 9.9e+02; ive 0; Mismatches 7;
                                              ب
                                            112
TAG_LIB=UI-R-CT0
TAG_TISSUE-rat brain pool
TAG_SEQ-ACTTC"
1 91 c 154 g 112
                                                                                                                                                                    1 ctatatccaccatatccccttccccttgcgtg 33
                                                                                                                                                                                    113 CTATCTCCCCCCATGTCCCCATGCCCTTCCCTG 81
                                           154 g
                                                                                                       Query Match 58.9
Best Local Similarity 78.8
Matches 26; Conservative
                                            121
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AI575981/c
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Gaps

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ò g RESULT 12 BG381507/c

Conservative

BASE COUNT

/strain="Strains" ratus not vegicus
/strain="Strains" ratus not vegicus
/db_xref="taxon:10116"
/clone="ur-FcT0-buk'b-05-0-UI"
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/clone_"ur-FcT0-buk'b-05-0-UI"
/clone_"ur-FcT0-buk'b-05-0-UI"
/dev_stage="ADULT"
/lab_host="bulub (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CT0
library is a normalized library constructed from the
following rat brain tissues: embryonic day 19, embryonic
day 19, embryonic day 21, adult day 1, adult day 12, adult
day 75, adult day 200. For a detailed description of the
library from which this clone was derived, please visit
our web site at ratest.eng.ulowa.edu. The subtraction has
been previously described in (Bonaldo, Lennon and Soares,

/organism="Rattus norvegicus"

Location/Qualifiers

us-09-721-543a-16.rst

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BE965057 916 bp mRNA linear EST 14-DEC-2000 601658842R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886043 3', mRNA sequence.
BE965057.2 GI:11769034
                          Song, H., Peng, Y., Gu, Y., Yang, Y., Gao, G., Xlao, H., Xu, X., Ll, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, Y., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Ye, M., Zhang, Q., Han, Z., Chen, Z., Hu, R. and Chen, J., Han, Z., Chen, Z., Hu, R. and Chen, J., Homo sapiens NPD library cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 916)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: 1.ife Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution and be
                                                                                                                                                                  Contact: Qinghua Zhang
Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64370045(ex.663332)
Fax: 86-21-6443206
Email: mbshi@ms.stn.sh.cn
This clone is available at Shanghai Hematology Institute in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
On Oct 3, 2000 this sequence version replaced gi:10575762.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                                                                                                                                                                      Chinese National Human Gencme Center at Shanghai
351 Guo Shoujing Road, Zhargjiang Hi- Tech Park, Pudong.
Location/Qualifiers
1. -696
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http://image.llnl.gov
Plate: LLCM649 row: d column: 12
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Pred. No. 1.1e+03;
0; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9£06"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="pituitary"
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1. .916
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         (bases 1 to 696)
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Best Local Similarity 78.8°
Matches 26; Conservative
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BE965057/c
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                                                                                                                   TITLE
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COMMENT
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Sprague_Daniegy_costs / strain="Sprague_Daniegy_costs / strain="Sprague_Daniegy_costs / strain="Sprague_Daniegy_costs / strain="Ur-R-G0-ur-b-11-0-UI"
/clone_lib="Ur-R-G0-ur-b-11-0-UI"
/clone_lib="Ur-R-G0-ur-b-11-Not I: Site_2: Eco RI; The UI-R-G0 polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-G0 library is a normalized library constructed from a mixture of rat tissues (nodose ganglia, dorsal root ganglia, and trigeminal ganglia). The tag is a string of 6 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaddo, Lennon and Soares, Genome Research 6: 791-806 , 1996."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Figure 1: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NoII site and the oligo-dT track served to verify it as a clone from the normalized ganglia library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                        Eukaryota; Mětazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                 Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , mRNA sequence.
                                                                                                                                                                                                                                                                                                                         97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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UI-R-G0-ur-b-11-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21.8; DB 9
Pred. No. 1e+03;
0; Mismatches

    .504
    /organism="Rattus norvegicus"

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                                                                                                                                                                                                                                                                                                      Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics (www.resgen.com)
Seg primer: M13 Forward.
Location/Qualifiers
                                               AI575981.1 GI:4560357
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78.8%;
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                                                                                                                     Rattus norvegicus
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                                                                                                                                                                                                                                                                                   discovery
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                   AUTHORS
TITLE
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COMMENT
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Gaps

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Search completed: June 4, 2002, 17:09:16 Job time: 4549 sec

, Appl , Appl Appli

Sequence 3 Sequence 2 Sequence 2 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1

Sequence

Sequence Sequence Sequence Sequence

1

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APPLICANT: Heimbrook, David C.
APPLICANT: Hoyle, Mona I.
APPLICANT: Oliff, Allen I.
TITLE OF INVENTION: E 2F-2, A NOVEL MAMMALIAN TRANSCRIPTION
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
               US-09-438-142-1
US-09-031-962D-5
US-08-522-942-1
US-08-222-617A-34
US-08-222-617A-24
US-08-946-914-25
US-09-224-110-15
US-09-224-110-15
US-09-276-914-1
US-09-347-803-19
                                                                                                                                                                                                                                                                 PCT-US94-07040-10
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US-08-742-026-22
US-08-117-362-32
                                                                                                                                                                                                                                              US-08-082-844-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5: David A. Muthard
P.O. Box 2000, 126 Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20.2; DE
Pred. No. 16;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MALHALD, DAVID:
REFERENCE/DOCKET NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 19042
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-4720
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1314 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-136-119-1/c

Sequence 1, Application US/08136119

; Patent No. 5473056

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.8%;
Matches 25; Conservative
STREET: P.O. I
CITY: Rahway
STATE: N.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ANTI-SENSE:
US-08-136-119-1
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                                                                                                                           June 4, 2002, 17:47:26; Search time 116.71 Seconds (without alignments) 77.872 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 7, App Sequence 13, App Sequence 13, App Sequence 4, App Sequence 4, App Sequence 4, App Sequence 4, App Sequence 3, App Sequence 4, App Sequence 6, App Sequence 1, App Sequence 2, App Sequence 3, App Sequence 3, App Sequence 3, App Sequence 4, App Sequence 4, App Sequence 4, App Sequence 5, App Sequence 6, 
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Sequence 2
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Sequence 3
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'cgn2_6/ptodata//ina/5A_COMB.seq:*
'cgn2_6/ptodata/1/ina/5B_COMB.seq:*
'cgn2_6/ptodata/1/ina/6A_COMB.seq:*
'cgn2_6/ptodata/1/ina/RB_COMB.seq:*
'cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
'cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
'cgn2_6/ptodata/1/ina/Packfiles1.seq:*
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-481-814A-2
US-08-845-998-3
US-08-09-206-537-3
US-09-206-537-3
US-09-206-537-3
US-08-206-176-7
US-08-206-176-7
US-08-166-13-182-13
US-08-466-603-4
US-08-466-717-4
US-08-466-717-4
US-08-466-717-4
US-08-466-717-4
US-08-466-717-3
US-08-998-416-416
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                                                                                                                                                                                                                                                                                                                                        383533 seqs, 122816752 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                         - nucleic search, using sw model
                                                                                                                                                                                                                                                                               IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                         US-09-721-543A-16
37
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length: 2000000000
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2259
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6763
10807
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Match 1
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Minimum DB Maximum DB

Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

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Gaps

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Indels

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Score 20.2; DB 1; Length 2647; Pred. No. 18; 0; Mismatches 8; Indels 0;
                                                                                       STREET: D.O. Box 2000, 126 Lincoln Avenue
CITY: Rahway
STATE: N.J.
COUNTRY: USA
21P: 07065-0907
COMPUTER READABLE FORM:
MEDIUW TYPE: FORM:
MEDIUW TYPE: FORM:
MEDIUW TYPE: FORM:
MEDIUW TYPE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,119
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRECOMMUNICATION NUMBER: 19042
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Coulie, Pierre G.
APPLICANT: Coulie, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Boon, Thierry
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
   NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Muthard
STREET: P.O. Box 2000, 126 Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 atccaccatatcccttcccttgcgtgtggg 37
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APPLICATION NUMBER: US/08/845,998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08845998
Patent No. 5879892
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NAME: Van Amsterdam, John R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2647 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 54.6%;
Best Local Similarity 75.8%;
Matches 25; Conservative (
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
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STREET: bov.
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; MOLECULE TYPE:
US-08-136-119-3
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ZIP: 02210
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STATE: MA
COUNTRY: U
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US-08-845-998-3
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APPLICANT: Hoyle, Mona I.
APPLICANT: Oliff, Allen I.
IITLE OF INVENTION: E 2F-2, A NOVEL MAMMALIAN TRANSCRIPTION
TITLE OF INVENTION: FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1766
                                                                                                                                               RESULT 2
US-08-481-814A-2/C
US-08-481-814A-2/C
Sequence 2, Application US/08481814A
Fatent No. 5869040
GENERAL INFORMATION:
APPLICANT HOU, Yen-Wing
TITLE OF INVENTION: GENE THERAPY METHODS AND COMPOSITIONS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: 12
ADDRESSEE: Blogen, Inc.
STREET: 14 Cambridge Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Floppy disk
COMPUTER: IBM Floppy disk
COMPUTER: IBM Floppy Misk
COMPUTER: IBM Floppy Misk
COMPUTER: IBM Floppy Misk
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,814A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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                                  339 ATCCACTCTGATGCACTTCCCCTTGGGGGTTGG 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATION: 429.1739

COTHER INFORMATION: /product= "E2F-2"

US-08-481-814A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Cambridge
STATE: Massachusetts
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Kaplan, Warren A
REFERENCE/POCKET UNBEER: A001
TELEPHONE: 617-679-2800
TELEPHONE: 617-679-2808
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1766 Dase pairs
LENGTH: 1766 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08136119
Patent No. 5473056
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: HeLa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.8'
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: mat_peptide LOCATION: 429..1739
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US-08-136-119-3/c
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Gaps

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19.4; DB 4; Length 2259; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
APPLICANT: Lucas, Sophie
APPLICANT: Lucas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2139 CCACCCTGAGCCCCTTCCCCTTTCTTGAG 2167
                                                                                                                                                                                                                                                                                                                                                                                                                                7 ccacccatatcccttccccttgcgtgtg 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRICR APPLICATION BATA:
APPLICATION NUMBER: 08/845,998
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09430854 Patent No. 6271019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Van Amsterdam, John R. REGISCRATION NUMBER: 40,212 REFERENCE/DOCKET NUMBER: LOJ TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.4%;
79.3%;
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INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617)720-3500
TELEFAX: (617)720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2259 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-CENICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                          HYPOTHETICAL: NC
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ns
                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 600
CITY: Bosto
STATE: MA
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FEATURE:
                                                                                                                                         ; NAME/KEY:
; LOCATION:
US-09-206-537-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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US-09-430-854-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-09-430-854-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09206537
Patent No. 6130052
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.4%; Score 19.4; D
79.3%; Pred. No. 36;
Live 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,998
FILING DATE:
ATTORNEY/AGENT INPORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEPHONE: (617)720-341
INFORMATION FOR SEQ ID No: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2259 base pairs
TENGTH: 2259 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 2139 CCACCCTGAGCCCTTCCTTCTTGAG 2167
             40,212
3R: L0461/7008
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REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L046;
TELECOMMUTICATION INFORMATION:
TELEPHONE: (617)720-244
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2259 base pairs
TYPE: nucleic acid
STRANDENESS: double
TOPLOGY: linear
MOLECULE TYPE: CONA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 79.34
Matches 23; Conservative
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COUNTRY: US
ZIP: 02210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
US-08-845-998-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
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US-08-756-506-5/C

Sequence 5, Application US/08756506

Patent No. 5905185

GENERAL INFORMATION:

APPLICANT: Garner, Ian

APPLICANT: Temperley, Simon M.

APPLICANT: Foster, Donald C.

APPLICANT: Freetr, Donald C.

APPLICANT: Freetr, Donald C.

APPLICANT: Freetr, Donald C.

APPLICANT: Prunkard, Donna E.

TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC

TITLE OF INVENTION: ANIMALS

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SISTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
FILING DATE:
                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/206,176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.4%; Score 19.4;
1larity 79.3%; Pred. No. 46
Conservative 0; Mismatche
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                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEPHONE: 206-548-2329
INFORMATION FOR SGO ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                   CORRESPONDENCE ADDRESS:
ADDRESSEE: 2ymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
CLONE: ovine beta-lactoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 10807 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                    ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98102
COMPUTER READABLE FORM:
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CLASSIFICATION: 435
    NUMBER OF SEQUENCES:
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Best Local Similarity
Matches 23; Conserv
                                                              STREET: 4225 R
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
                                                                                        Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seattle
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Sequence 7, Application US/08206176
Patent No. 563940
GENERAL INFORMATION:
APPLICANT: Carner, Ian
APPLICANT: Prunkard, Donna E
APPLICANT: Prunkard, Donna E
TITLE OF INVENTION: Production of Fibrinogen in Transgenic TITLE OF INVENTION: Animals
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                 APPLICANT: Garner, Ian
APPLICANT: Cottingham, Ian R.
APPLICANT: Temperley, Simon M.
APPLICANT: Temperley, Simon M.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Donna E.
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
TITLE OF INVENTION: ANIMALS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
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Mismatches
                                                                2139 CCACCCTGAGCCCCTTCCCCTTTCTTGAG 2167
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                                          7 ccacccatatccccttccccttgcgtgtg 35
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STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 95-28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                       Sequence 23, Application US/08756506
Patent No. 5905185
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 206-442-6678 INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 52.4%;
Best Local Similarity 79.3%;
Matches 23; Conservative (
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Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: S
STATE:
Matches
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Pred. No. 46; 0; Mismatches

DB 1; Length 10807;

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Gaps
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Patent No. 5726018
GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
APPLICANT: Kuhajda, Francis P.
TITLE OF INVENTION: No. 5726018el Mammalian Protein Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Codon also can encode Thr NAME/KEY: misc_feature
LOCATION: (729)
OTHER INFORMATION: Codon also can encode Ile
NAME/KEY: misc_feature
LOCATION: (1092)
OTHER INFORMATION: Codon also can encode Val
NAME/KEY: misc_feature
LOCATION: (1191)
                                             CONTROL (495)

OTHER INFORMATION: Codon also can encode lle (495)

OTHER INFORMATION: Codon also can encode lle LOCATION: (510)

OTHER INFORMATION: Codon also can encode Ala MAME/KEY: misc_feature

LOCATION: (550)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Codon also can encode lle
NAME/KEY: misc_feature
LOCATION: (1284)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Codon also can encode Glu
NAME/KEY: misc_feature
LOCATION: (1293)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Codon also can encode Ala
NAME/KEY: misc_feature
LOCATION: (1296)
OTHER INFORMATION: Codon also can encode Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (1308)
OTHER INFORMATION: Codon also can encode Gly
          LOCATION: (486)
OTHER INFORMATION: Codon also can encode Ser
                                                                                                                                                                                                                                                    OTHER INFORMATION: Codon also can encode Val
                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Codon also can encode Glu
                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Codon also can encode Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (621)
OTHER INFORMATION: Codon also can encode Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Codon also can encode Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Codon also can encode Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Codon also can encode Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 tatatccacccatatccccttccccttgcgtg 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 TITATGIACCTACGICCCTTCCCCTTACGGG 86
                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (588)
                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (714)
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LOCATION: (1287)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (1290)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1302)
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
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US-08-466-603-4
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Patent No. 6294653

GENERAL INFORMATION:

APPLICANT: Mayfield, Stephen

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT MOLECULES

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT MOLECULES

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT MOLECULES

FILE REFERENCE: SCR21775

CURRENT APPLICATION NUMBER: US/09/613,182

CURRENT APPLICATION NUMBER: 05/341,550

PRIOR PLILNG DATE: 1999-07-13

PRIOR FILING DATE: 1999-07-13

PRIOR FILING DATE: 1999-07-13

PRIOR PLILING DATE: 1999-01-17

PRIOR PLILING DATE: 1997-01-17

PRIOR PLILING DATE: 1997-12-12

PRIOR PLILING DATE: 1997-12-12

SOFTWARR: PLEATION NUMBER: 60/059,400

PRIOR FILING DATE: 1997-12-12

SOFTWARE: PLING DATE: 1997-12-12

SOFTWARE: PLING DATE: 1997-12-12
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (252)..(1310)
NAME/KE: MAISC_feature
LOCATION: (279)
OTHER INFORMATION: Codon also can encode Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION: Codon also can encode Asn
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 52.4%; Score 19.4; D
Best Local Similarity 79.3%; Pred. No. 46;
Matches 23; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Codon also can encode Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION: Codon also can encode Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Chlamydomonas reinhardtii
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SAWISHEK, DEDOTAH A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 95-28
TELECHONE: 206-442-6672
TELEPHONE: 206-442-6678
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10807 base pairs
TYPE: nucleic acid
STRANBORDES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: m1sc_feature
LOCATION: (282)
OTHER INFORMATION: Codo
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                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-613-182-13/c
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Sequence 4, Application US/08468066

Patent No. 575676

GENERAL INFORMATION

APPLICANT: Pasternack, Gary R.

APPLICANT: Ruhajda, Francis P.

TITLE OF INVENTION: Uncontrolled Cell Division

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSE: Banner, Birch, McKie & Beckett

STREET: 1001 G Street, N.W.

CIT: Washington, D.C.

STATE: District of Columbia

21P: 20001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 759;
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APPLICATION NUMBER: US/08/468,066 FILING DATE: 06.JUN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,503
  Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 51.4%; Score 19; DB Best Local Similarity 81.5%; Pred. No. 44; Matches 22; Conservative 0; Mismatches
                                      APPLICATION NUMBER: US/08/314,503A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POSOT3KE ESQ., LAURENCE H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECHONE: 202 508-9153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERNCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION:
TELEPHONE: 202 508-9153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ctatatccacccatatccccttcccct 27
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: POSOTSKE ESG., Lau
                                                                                                                                                                                                                                      TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 759 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                         CURRENT APPLICATION DATA:
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MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3..548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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US-08-314-503A-4
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US-08-468-066-4
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Sequence 4, Application US/08314503A

Sequence 4, Application US/08314503A

Sequence 4, Application US/08314503A

SEQUENCE 1 INFORMATION: Uncontrolled Cell Division

TITLE OF INVENTION: Uncontrolled Cell Division

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner, Birch, McKie & Beckett

STREET: 1001 G Street, N.W.

CITY: Washington, D.C.

STATE: District of Columbia

21P: 20001
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                                                                                                                                             COUNTRY: U.S.A.

ZIP: 20001

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,603
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,503
TITLE OF INVENTION: Uncontrolled Cell Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19; DB 1;
Pred. No. 44;
               NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 101G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
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NAME: POSOTSAKE ESQ., Lautence H.
RECISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELEPHONE: 202 508-9153
TELEPHONE: 202 508-9299
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COMPUTER FIGURE

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 759 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 51.4%;
Best Local Similarity 81.5%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION:
US-08-466-603-4
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APPLICANT: Pasternack, Gary R.
APPLICANT: Kuhajda, Francis P.
TITLE OF INVENTION: No. 6040173el Mammalian Protein Associated With TITLE OF INVENTION: Uncontrolled Cell Division NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTE: DISTRICT OF COLUMBIA COMPUTER: STATE: DISTRICT OF COMPUTER SYSTES OF C
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Pred. No. 44;
0; Mismatches 5; Indels
                                                  DB 2; Length 759;
                                                                                                                                 5; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,743
FILING DATE:
                                             Query Match 51.4%; Score 19; DB Best Local Similarity 81.5%; Pred. No. 44; Matches 22; Conservative 0; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: POSOTSKE ESG., LAUVENCE H.
REGISTRATION NUMBER: 34,696
REFERENCE/DOCKET NUMBER: 1107.4721
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.508-9153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/314,503
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81.58;
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SEQUENCE CHARACTERISTICS:
LENGTH: 759 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 81.5
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 508-9299
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MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3..548
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US-08-466-743-4
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| Sequence 4, Application US/08466717 |
| Sequence 4, Application US/08466717 |
| Patent No. 5874234 |
| Patent No. 5874234 |
| APPLICANT: Pasternack, Gary R. |
| APPLICANT: Kuhajda, Francis P. |
| TITLE OF INVENTION: Uncontrolled Cell Division |
| WUMBER OF SEQUENCES: 9 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Banner, Blrch, McKie & Beckett |
| STREET: 1001 G Street, N.W. |
| CITY: Washington, D.C. |
| STATE: District of Columbia |
| COUNTRY: U.S.A. |
| CITY: ACOUNTRY: U.S.A. |
| CI
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MEDIUM TYPE: Floppy disk
COMPUTER: Elbopy disk
COMPUTER: Elb PC compatible
OPERATING SYSTEM: PC-DOS/AKS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,717
FILING DATE: 06-JUN-1995
PIOR APPLICATION 1435
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 08/314,503
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19; DB 1
Pred. No. 44;
0; Mismatches
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NAME: POSOTSKE ESQ., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION:
TELECHONE: 202 508-9153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ctatatccaccatatccccttcccct 27
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Best Local Similarity 81.5%;
Matches 22; Conservative C
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SEQUENCE CHARACTERISTICS:
LENGTH: 759 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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LENGTH: 759 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Mus sp
                                                                                                                                                                                           MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Mus sp
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US-08-468-066-4
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; LOCATION:
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Human immune/haema

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e mapping; gene mapping; gene therapy; forensic; medical imaging; diagnostic; genetic disorder; ss.
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AAA52780
AAA33403
AAA33403
AAA59826
AAA6609
AAX30975
AAX30975
AAX36138
AAS86138
AAS86138
ABL22366
AAS69432
AAS94024
AAS77690
                                             AAK69540
AAQ86483
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AAS18560
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ABL07082
ABA70980
ABA37400
ABA19256
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23-AUG-2000; 2000US-0649167
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P-PSDB; ABG05222.
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food supplement;
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Human polynucleoti
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(without alignments)
121.814 Million cell updates/sec
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1 ctatatccaccatatcccttcccttgcgtgtggg 37
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Compugen Ltd
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                                                                                                                                                                                                         1736436 seqs, 858457221 residues
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           GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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AAH15189
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Gapop 10.0 , Gapext 1.0
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New isolated polynucleotide and encoded polypeptides, useful in

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PECR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags to relative processed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) and its binding antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as (II). (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical consorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in clasorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. As564197-As594564 represent novel human diagnostic coding sequences of the invention of the printed coding sequences of the invention of the printed coding sequence data for this patent did not appear in the printed constitution of the coding sequence data for this patent did not appear in the printed constitution of the coding sequence data for this patent did not appear in the printed constitution of the coding sequences of the invention of the coding sequence data for this patent did not appear in the printed coding sequences.
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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                         Claim 1; SEQ ID No 5213; 103pp; English
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P-PSDB; ABG29789.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerises are also used in diagnostics as expressed sequence tags confinentifying expressed genes. (I) is useful in gene therapy techniques confinentifying expressed genes. (I) is useful in gene therapy techniques confinentifying expressed generating antibodies against it, detecting or confinence of a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and (II) and (II) are useful in medical maging of sites expressing (II). (II) and (II) are useful in medical confiscers involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in clasometric for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cand confine sequences of the invention.

Conditional sequences of the invention.

Conditional for man for an electronic format directly from Wibo the invity in the printed conficultion int/pub/published_pct_sequences.
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responsible for genetic disorders or other traits and to assess blodiversity \ \cdot \ 
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11ve 0; Mismatches 8;
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Coding sequences AAS64197-AAS94564 represent novel human DNA and clasmostic coding sequences of the invention.

Codes the sequence data for this parent did not appear in the printed specification but was obtained in electronic format directly from WIPO
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A, Nagai K, Otsuki T;
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Pred. No. 21;
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                                                                                  Claim 1; SEQ ID No 29833; 103pp; English,
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Sugiyama T, Wakamatsu
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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Best Local Similarity 77.1%;
Matches 27; Conservative
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the comprementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 5'-end sequence and an oligonucleotide comprises a 5'-end sequence and an oligonucleotide comprises a 5'-end polynucleotide which comprises a 1'-end sequence. Where the oligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence. A'-end sequence and sequence and sequence and sequence at least 15 nucleotides and the combination of the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length and AHI13631 to AAHI3742 represent human cDNA sequences; AABS2446 to AAHI3632 AABS3831 represent human amino, acid sequences; and AAHI3629 to AAHI3632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represent oligonucleotides, all of which are used in the exemplification
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and/or diagnosis of the abnormality of the proteins encoded by the
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57;
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                                                                                                              Claim 8; SEQ ID 13279; 2537pp + CD ROM; English.
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0; Mismatches
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82.8%; Pred. No. 5
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Best Local Similarity 82.8%
Matches 24; Conservative
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                                    full-length cDNAs
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At The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of genes in one or more second filamentous fungal cells. The method uses fluorescence—labeled nucleic acids isolated from the Fr cells and a substrate of expressed sequence tags (EST). The ESTS care used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring che global expression of genes from FF cells allows the production potential of the mcroorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be conditiced and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore adapt to changes in culture conditions, environmental stress, spore confineating. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an example of the results. AAFI1248 to AAFI1487 represents ESTS from Aspergillus or parents and satisficant and satisficant are confineating. AAFI1248 to AAFI1487 represents ESTS from AAFI4875 to Transpace and in the present invention.
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Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -
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78.1%; Pred. No. 55;
:ive 0; Mismatches
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2000US-0654936.
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27-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoicsis regulating activity, tissue growth factor activity, immunomodulatory activity and activity insue growth factor activity, immunomodulatory activity and activit/inhibin activity and may be useful in the diagnosis and/or the activity and activity and activity and activity and activity and activity and may be useful in the diagnosis and/or the activity and activ
                                                                                                                   Ma Y;
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                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                   Cao Y,
                                                                                                             Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y,
Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 56.2%; Score 20.8; DB 22; Length 1462; Best Local Similarity 78.1%; Pred. No. 62; Matches 25; Conservative 0; Mismatches 7; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding novel human diagnostic protein #5214.
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                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 837-838; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                 useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS69410 standard; cDNA; 1452 BP
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30-NOV-2000; 2000US-0728422
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                                                                                                                                                                                                                              WPI; 2001-476283/51.
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                                                        (HYSE-) HYSEQ INC.
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                                                                                                             Tang YT,
Zhao QA,
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AAS69410
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The colymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The color identifying expressed genes. (I) is useful in gene therapy techniques correstore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or guantitating a polypeptide in tissue, as molecular weight markers and as (II) and its binding partners are useful in medical imaging of sites expressing (II) and its binding partners are useful in medical imaging of sites expressing (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in clasorates, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cannon acid sequences. Ansoldly-Ansoldsely represent novel human classequences of the invention.

Consideration but was obtained in electronic format directly from WIPO considerations of the consideration of mutations of the consideration of mutations of the consideration of mutations of the invention.
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food supplement; medical imaging; diagnostic; genetic disorder; ss.
                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1452 BP; 370 A; 331 C; 367 G; 384 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding novel human diagnostic protein #29825.
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                                                                                                                          Claim 1; SEQ ID No 5214; 103pp; English.
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74.3%;
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23-AUG-2000; 2000US-0649167
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Best Local Similarity 74.39
Matches 26; Conservative
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                                                                                   biodiversity
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polypeptide (II) sequences. (I) is useful as hybridisation probes, and polymersae chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to man application of mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                       and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this putent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                  diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
New isolated polynucleotide and encoded polypeptides, useful in
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                                                                                                                                The invention relates to isolated polynucleotide (I) and
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0; Mismatches
                                                                                            Claim 1; SEQ ID No 29825; 103pp; English:
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Best Local Similarity 74.3
Matches 26; Conservative
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                                                        biodiversity
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                                                                                                                                         The invention relates to isolate polymorate (i) and the polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polymorleotides are also used in disponsition as expressed sequence tags. for identifying expressed genes. (I) is useful in gene therapy techniques. (I) recombinant activity of (II) or useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful in medical imaging of sites expressing (II). (I) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in capponshible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences. Ass&4197.AAS&4564 represent novel human and dispensitic coding sequences of the invention of mutations captainted in the sequence data for this patent did not appear in the printed construction of the construction of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
    diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                  relates to isolated polynucleotide (I) and
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0; Mismatches
                                                                                   Claim 1; SEQ ID No 26967; 103pp; English.
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74.38;
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11-JUL-2000; 2000US-0614150
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Matches 26; Conservative
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                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
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Claim 1; SEQ ID NO 18571; 21pp + Sequence Listing; English.
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Best Local Similarity 74.3
Matches 26; Conservative
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                                                                                                                                                                                 (ABB57737-ABB72072)
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quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence date for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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0; Mismatches
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hes 26; Conservative
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a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

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imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 7903;
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7903 BP; 2316 A; 1835 C; 1850 G; 1902 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20.6; DB
Pred. No. 92;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 atatccacccatatccccttccccttgcgtggg 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK69540 standard; DNA; 13094 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 55.7%;
Best Local Similarity 74.3%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0218290.
2000US-0220963.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-2001; 2001WO-US01354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0225757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2001 (first entry)
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24-FEB-2000;
02-MAR-2000;
17-MAR-2000;
17-MAY-2000;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK69540;
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us-09-721-543a-16.rng

8 cacccatatccccttccccttgcgtgtggg 37

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Ruben SM;
                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                           05-JAN-2001; 2001US-0259678.
                      2000US-0249208
                                           2000US-0249212
                                                                                                                               2000US-0250391
                                                                                                                                                2000US-0256719
                                                                                                         2000US-0249297
                                                                                                                                                                                                                 Barash SC,
                                                                                                                                                                                                                            WPI; 2001-483426/52
         08-NOV-2000;
17-NOV-2000;
                                                                                           17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                             01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
                                                                                                                                              05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                     08-DEC-2000;
                                                                                                                         01-DEC-2000;
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                                                                                                                                                                                    11-DEC-20
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5298 CACCCCCATCCCCACCCCTCGAGTGTGGGG 5269
                                                                                                                          AAQ86483 standard; cDNA; 2647
                                                                                                                                                                     AAQ86483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM81370 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
cample, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
cappression by rectifying mutations or deletions in a patient's genome
cut that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
colynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54921 co AAK54950 and AAM82169
represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 24352; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13094 BP; 2675 A; 3841 C; 4019 G; 2559 T; 0 other;
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Heimbrook DC, Ivey-Hoyle M, Oliff AI;

WPI; 1995-141220/19. P-PSDB; AAR71734.

(MERI) MERCK & CO INC

13-OCT-1993;

94GB-0020283. 93US-0136119

/*tag= a /product= E2F-2 transcription factor.

GB2282814-A 19-APR-1995

Location/Qualifiers 429..1683 /*tag= a

E2F-2; transcription; factor; regulation; cell cycle; retinoblastoma; tumour; suppressor; ss.

Homo sapiens

Key

Human transcription factor E2F-2 cDNA.

(first entry)

23-NOV-1995

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                           involved in cell cycle regulation. In particular binding of E2F to the retinoblastoma gene product (PRD) causes down regulation of the transcription of any genes containing the E2F binding site. E2F-2 is useful in the study of cell cycle regulation especially in the study
                                                                                                                                                                                                AAQ86483 codes for the human transcription factor E2F-2. E2F-2 is
regulation and useful for drug screening, also related cDNA, plasmids and transformed cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                of pRb and certain viral oncogenes and oncoproteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 54.6%: Score 20.2; DB 16;
Local Similarity 75.8%; Pred. No. 1.1e+02;
Local 25; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        767 ATCCACTCTGATGCACTTCCCCTTGGGGGTTGG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 atccacccatatccccttccccttgcgtgtggg 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: June 4, 2002, 17:56:36
Job time: 7114 sec
                                                                                                                                 Claim 3; Page 30-31; 53pp; English.
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Matches
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Gaps

55.1%; Score 20.4; DB 22; Length 13094; 80.0%; Pred. No. 1.2e+02; Live 0; Mismatches 6; Indels 0;

24; Conservative

Matches

Best Local Similarity

Query Match

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Rattus

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Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Minimum DB s Maximum DB s

Database

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DNA linear HTG 21-DEC-2001
2, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
Eukaryota; Metazoa; Chordatu; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Malsbrooks, S.L., Amaratunge, H.C., Are, J.R., Barbarta, J., Balsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbarta, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Biwad, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus clone CH230-175N2, ***, 64 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                   AC013680
AC069172
HUAC002038
                                                                                                                                                                                                                                                          HSY237C10_1
AC040954
                                                                                                                                                            AC101433
AC026569
AC022394
AP000553
AC018751
                                                                                                                                      AC102828
AC102828
AC101896
                                                                                                                                                                                                    AC009516
AC096736
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AC025854
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                                                                                       AC094327
                                                                                                                                                                                                                                                                                                                                           MMRP1
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HTG: HTGS_PHASE1.
Norway rat.
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162301
180446
128481
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37959
49804
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147521
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146187
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170359
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154062
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1210
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188872
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                                                                                                                                                                                                    169237
Rattus.
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
AC098141
                                                       ν., <u>144,</u>
                                                                                                                                                                                                                                                 ٠, ٠,٠
                                                   June 4, 2002, 17:48:43; Search time 2137.99 Seconds (without alignments) 362.154 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                            3595312
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                    1 ctatatccacccatatccccttccccttgcgtggg
                                                                                                                                           1797656 segs, 10463268293 residues
                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                      - nucleic search, using sw model
                                                                                                                             Gapop 10.0 , Gapext 1.0
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em_htg_inv:*
em_htg_other:*
em_htgo_inv:*
                                                                                 US-09-721-543A-16
37
                                                                                                                                                                            seq length: 0
seq length: 200000000
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gb_un:*
gb_vi:*
em_ba:*
em_fun:*
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Description

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Query Match Length DB

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Result

AC013680 Homo sapi AC065172 Homo sapi AC002038 Homo sapi AC097080 Rattus no AC080124 Homo sapi AC020760 Homo sapi AL133173 Human DNA Y07941 M.musculus

AL451050 Human DNA AC025864 Homo sapi

AP000546 Homo sapi AC105064 Mus muscu AP001860 Homo sapi Continuation (2 of AC040954 Mus muscu AC083826 Homo sapi AC013680 Homo sapi

AC091474 MUS MUSCU AC102828 MUS MUSCU AC101433 MUS MUSCU AC25559 HOMO Sapi AC0255394 HOMO Sapi AC018751 HOMO Sapi AC018751 HOMO Sapi AC018751 HOMO Sapi AC095716 HOMO Sapi AC095718 Romo Sapi AC095718 Rattus norv

AC018751 H AC009516 H AC096736 H AC094163 F

Homo sapi Rattus no Rattus no Homo sapi

AC079586 AC011023 AC011033 AC094327 AC094327 AC093959 AC093959 AC091474 AC102828 AC102828

Rattus no

Human DNA

Homo sapi Homo sapi Homo sapi Homo sapi Homo sapi Homo sapi Homo sapi

AL163280 | AP001791 | AC013732 |

AF064860 AC018807

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Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagy, N., Ford, J.,
Foster, P., Frantz, P., Gabisi, A., Gaora, M., Gunaratne, P., Hale, S.,
Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
Hollins, B., Homsi, F., Howard, S., Huber, J., Hulpk, S., Hume, J.,
Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Katovito, J., Kureshi, A., Ludry, N., Leal, B., Lewis, L.
Luulseged, H., Lozado, R.J., Lu, X., Lutced, M. P., Maedor, M.,
Martinez, E., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M.,
Martinez, E., Massey, E., Mawhiney, E., Mitchell, T., Mohabbat, K.,
Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N.,
Nuyyen, A., Nuyyen, N., Nuyen, N., Nucleos, M., Pace, A., Payton, B.,
Peery, J., Percers, L., Petcens, R., Primus, E., Put, L.,
Oulles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M.,
Stone, H., Sutton, A., Svatek, A., Tamerisa, A., Tamerisa, K.,
Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N.,
Thomas, S., Usman, K., Wasquez, L., Vera, V., Villalon, D., Vinson, D.,
Wallington, S., Williams, G., Williamson, A., Washington, C.,
Wallington, S., Williams, G., Williamson, A., Washington, C.,
Weinstock, G. and Gibbs, R.
Phases, I., Rayan, R.
Phases, I., Rayan, R.,
Weinstock, G., and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 64 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 152722 bases at least Q40 Consensus quality: 15678 bases at least Q30 Consensus quality: 163676 bases at least Q30 Estimated insert size: 156476; sum-of-contigs estimation Quality coverage: Ox in Q20 bases; agazose-fp estimation Quality coverage: 2.6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 21, 2001 this sequence version replaced gi:16327847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11538: contig of 11538 bp in length
11638: gap of unknown length
24157: contig of 12519 bp in length
24257: gap of unknown length
29851: contig of 5594 bp in length
29951: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
Center project name: GGMO
Center clone name: CH230-175N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Baylor College of Medicine
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Direct Submission
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11639
24158
24258
29852
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REFERENCE
AUTHORS
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COMMENT

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of 2845 bp in length
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of 1445 bp in length
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 40205)
S Taudlen,S. and Rosenthal,A.
E 2 (bases 1 to 40205)
S Taudlen,S., Nordsiek,G., Dagand,E., Hildmann,T., Drescher,B., Weber,J., Rosenthal,A. and Yaspo,M.L.
Direct Submission
L Submitted (29-JAN-1998) Genome Analysis, Institut for Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
Location/Qualifiers
I. 40205
//Chromosome="Homo sapiens"
//Chromosome="21"
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AF045450.1 GI:2895783
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0; Mismatches
                              unknown
                                                                                                         of 1643
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167660: 0
167760: 9
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144999:
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150041:
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Matches 28; Conservative
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VERSION
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JOURNAL
REFERENCE
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AF045450
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Homo sapiens chromosome 21q22.3 PAC 206A10, complete sequence.
AF121782.1 GI:4210991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 142742)
Taudien,S., Dagand,E., Hildmann,T., Nordsiek,G., Drescher,B., Schattevoy,R., Weber,J., Schilling,M., Menzel,U., Yaspo,M.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Solution.

Borenthal, A.

Direct Submission

Submitted (11-7099) Genome Analysis, Institute for Molecular Submitted (11-7099) Bentenbergstrasse 11, Jena 07745, Germany

Location/Qualiflers

1. .142742
         complement(19501. .19881)
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/rpt_type=tandem
/rpt_tdence=not_experimental
20223. .20643
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; Pred. No. 60;
0; Mismatches
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/map="21q22.3"
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3. 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.0%;
Matches 28; Conservative
                                                                            repeat_region
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="GRAIL, score = 81.000%, comment = excellent shadow" /evidence=not_experimental complement(19379. .19399) /note="Xpound exon prediction, score = 60% (0%)"
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11015. 11944
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AF064860
AF064860.1 GI:3171153
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// Acte="General comment = Single-exon_gene 279 bp frame: 2 phase: 0" /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 165382)
Rump, A., Dagand, E., Hildmann, T., Nordsiek, G., Drescher, B., Weber, J., Schattevoy, R., Yaspo, M.-L. and Rosenthal, A. Direct Submission
Submitted (12-May-1998) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany Location/Qualifiers
                                       comment - good shadow"
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                       21150. .21275
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0
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/rpt_family="MLTIA1"
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complement(18397. .18584)
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complement(19228. .19361)
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ilarity 80.08;
Conservative (
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ACO18807 203715 bp DNA linear HTG 07-JUL-2000 Homo sapiens chromosome 8 clone RP11-648J12, WORKING DRAFT SEQUENCE, 25 unordered pieces.
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Waterston, R. H.
Direct Submission
Submitted (03-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 27, 2000 this sequence version replaced gi:7235308.
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Homosapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 203715)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                       Query Match 64.3%; Score 23.8; DB 9; Length 165382; Best Local Similarity 80.0%; Pred. No. 48; Astches 28; Conservative 0; Mismatches 7; Indels 0;
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Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site:http://genome.wustl.edu/gsc/index.shtml
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             3 atatccacccatatccccttccccttgcgtgtggg 37
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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    203715
    organism="Homo sapiens"

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Dukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Eutheleostomi; Bukaryota; Butherla; Primates; Catarrhini; Hominidae; Homo.

E. (bases I to 34000).

Bark, H. S., Toyoda, A., Ishii, K., Totoki, Y., Choi, D. K., Soeda, E., Ohki, W., Takagi, T., Sakaki, Y., Tauden, S., Blechschmidt, K., Polley, A., Menzel, U. Delabar, J., Kumpf, K., Iehmann, R., Patterson, D., Reichwald, K., Rumpf, A., Schillhabel, M., Schudy, A., Zimermann, W., Rosenthal, A., Kumpf, K., Mitsuyama, S., Antonarakis, S. E., Minoshima, S., Shinizu, N., Nordsidk, G., Hornischer, K., Brandt, P., Schafe, M., Schoen, O., Desario, A., Riages, S., Hennig, S., Riesselmann, L., Dagand, E., Welrmeyer, S., Borzym, K., Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. end
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Homo sapiens chromosome 21 segment HS21C080.
AL163280 AP001735 BA000005
AL163280.2 GI:7717369
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      mRNA
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                                                                                                                                                                                                                                                                                                                                                                                              * Keio University School of Medicine, Dept. of Molecular Biology, * Tokyo 160-8882, Japan, * e.mail: shimizu@dmb-med.keio.ac.jp * URL: http://adenine.dmb.med.keio.ac.jp/
Direct Submission
Submitted (05-MAY-2000) The Chromosome 21 Mapping and Sequencing
Consortium: * RIKEN Genomic Sciences Center, Human Genome Research
Group * Institute of Molecular Biotechnology, Genome Analysis *
Kelo University School of Medicine, Dept. of Molecular Biology *
GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular
Genetics (addresses see below)
                                                                                                                                                 The Chromosome 21 Mapping and Sequencing Consortium consists of **RIKEN Genomic Sciences Center, Human Genome Research Group, **Segamihara 228-8555, Japan, **e.mail: sakaki@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * GBF, Dept. of Genome Analysis,
* Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
info.genome@gbf.de
* URL: http://genome.gbf.de/
                                                                                                                                                                                                                                                                                     * Institute of Molecular Biotechnology, Genome Analysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Max-Planck Institute for Molecular Genetics,
Ihnestrasse 73, D-14195 Berlin, Germany,
e.mail: info-chr21@dolgen.mpg.de
URL: http://chr21.rz-berlin.mpg.de/.
Location/Qualifiers
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* e.mail: gscj-submit@genome.imb-jena.de
* URL: http://genome.imb-jena.de/
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....... 141605 bp DNA 11near HTG 18-FEB-2001
Homo supiens chromosome 2 clone RP11-550023, WORKING DRAFT
SEQUENCE, 9 unordered pieces.
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Submitted (13-NOV-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 17, 2000 this sequence version replaced g1:8961220.
                                                                                                                                                                                                                                                                                                                                                             Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 141605)
Waterston, R.H.
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                         Length 140000;
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Center code: WUGSC
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                                                            Indels
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                       6
                                                                                                                 Db 86668 TATATTCACCATATCCACTTCCTCTCTACTGTGGG 86703
                         DB
                                                                                             2 tatatccacccatatccccttcccttgcgtgtggg 37
                       Score 23.2; 1
Pred. No. 83;
                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of Homo sapiens clone Unpublished
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AC013732.6 GI:9838265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 141605)
Waterston, R.H.
                       Query Match 62.7%;
Best Local Similarity 77.8%;
Matches 28; Conservative
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AUTHORS
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1. (bases 1 to 140000)

1. Shattori, M., Ishli, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

1. Direct Submission

1. Submitted (11-APR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKRN), Genomic Sciences Center (GSC);

1.7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattoriggsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

On Dec 7, 2001 this sequence version replaced gi:9927282.
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Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 234299 ATGTCCTTCCATATTCCCTTCTCTTTGAGTGTGGG 234333
                               /rpt_family="SINE/Alu"
/rpt_type=DISPERSED
14013. 14131
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/rpt_rype=TANDEM
14561. 14598
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/rpt_family="Simple_repeat"
/rpt_family="Ciple_repeat"
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/rote="(TG)n"
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26034 c 24406 g 43663 t
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/rpt_type=TANDEM
15331. 15460
/gene="SH3BGR"
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complement(13598. .13892)
/note="AluY"
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/rpt_type=DISPERSED
complement(18013. .18312)
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/db_xref="taxon:9606"
/chromosome="11"
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/rpt_family="SINE/Alu"
/rpt_type=DISPERSED
18739. 19157
                                                                                                                                                                                                                                                                                                                                                         15427. .15460
/gene="SH3BGR"
16255. .16471
/note="AluSg/x"
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11 Similarity 80.0%;
28; Conservative
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FEATURES
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Ososjawa K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Cataneso, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                       Watersoum, Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Sep 18, 2001 this sequence version replaced gi:15145691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
4 (bases 1 to 148332)
Waterston, R. H.
Direct Submission
Submitted (18-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The clone RP11-207G14 contains a 3577 bp insertion not sequenced in the left neighboring clone, RP11-31G7. This insertion sequence is being submitted as H_NH0207G14_FI. Data from AC073088 was used to finish this clone, AC079586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-31G7, 2000 bp overlap; the clone sequenced to the right is RP11-323P8. Actual start of this clone is at base position 140492 of RP11-31G7; actual end is at base position 140492 of RP11-31G7;
                                                                                                                                                                                                                                                                                                                                         Center code: WÜGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: H_NH0207G14
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/organism="Homo sapiens"
//db_xref="taxon:9606"
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/rpt_family="ERV1"
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/rpt_family="L1"
1242. .1695
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Submitted (02-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo saplens BAC clone RP11-207G14 from 2, complete sequence.
AC079586
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Shah,N. and Kozlowicz,A.
The sequence of Homo sapiens BAC clone RP11-207G14
Upublished (2001)
3 (bases 1 to 148332)
Waterston,R.H.
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            67793: gap of unknown length
85670: contig of 17877 bp in length
85770: gap of unknown length
110614: contig of 24844 bp in length
110714: gap of unknown length
141605: contig of 30891 bp in length.
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8
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20025 .33364
/note="assembly_name:Contig9"
33465 .47072
/note="assembly_name:Contig10"
47173 .67693
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/note="assembly_name:Contig13"
110715. 141605
/note="assembly_name:Contig14
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Genome Res. 8 (11), 1097-1108 (1998)
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/note="assembly_name:Contig12"
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/note="assembly_name:Contig7"
10029. 19924
/note="assembly_name:Contig8
clone_end:SP6
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/note="assembly_name:Contig6"
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29167 c 28457 g 40051 t
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/db_xref="taxon:9606"
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Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                               /chromosome="2"
/clone="RP11-550023"
                                                                                                                                                      Location/Qualifiers
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77.88;
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Best Local Similarity 77.8%
Matches 28; Conservative
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Signature, and to 162301)

Baldwin, J., Barna, N., Beckerly, R., Boguslavkly, L., Bouchgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boguslavkly, L., Bouchgalter, B., Brown, A., Castle, A., Colangelo, W., Collins, S., Collymore, A., Cooke, P., Darallano, K., Dawar, K., Domino, M., Donolan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardynas, S., Grant, G., Rann, L., Karatas, A., Hotton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McEwan, P., McGurk, A., McKernan, K., Mcdaughlin, J., Maldin, J., Maylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Rilacy, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirtell, A., Vasailiev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Submitted (30-SEP-1999) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACO11023 162301 bp DNA 11near HTG 30-MAR-2000
Homo sapiens clone RP11.-115C16, WORKING DRAFT SEQUENCE, 8 unordered
pieces.
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Birren, B., Lintcon, L., Nusbaum, C. and Lander, E.
Homo saplens, clone RP11-115C16
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Best Local Similarity 77.8%; Pred. No. 82;
Matches 28; Conservative 0; Mismatches
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                                                                                                                    ..... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 30, 2000 this sequence version replaced gi:6573937. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 194000; agarose-fp
Insert size: 161601; sum-of-contigs
Quality coverage: 4.4 in Q20 bases; agarose-fp
Quality coverage: 5.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                    Center clone name: 115_C_16
Sequencing vector: M13; M77815; 100% of reads
Schemistry: Dye-terminator B19 Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 1570% bases at least Q40
Consensus quality: 1595% bases at least Q20
Consensus quality: 1595% bases at least Q20
                                                                                                                                                                                20177 20276: gap of 100 bp 20277 34761: contig of 14485 bp in length 34762 34861: gap of 100 bp 24862 63486 63585: gap of 100 bp 100 bp 63586 63585: gap of 100 bp 63586 63586 94394: contig of 30809 bp in length
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12357 20176: contig of 7820 bp in length
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/clone_lib="RPCI-11 Human Male BAC"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 180446)

1 Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Homo sapiens 180,446 genomic DNA of 11q

L. (bases 1 to 180446)

2 (bases 1 to 180446)

1 Antori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

Fujiyama,A., Yada,T., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

Fujiyama,A., Yada,T., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

L. Submitted (08-WAY-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,

Japan (E-mail:hattori@gsc.riken.go.jp,

Fax:81-42-778-9923,

On May 30, 2000 this sequence version replaced g1:7769922.
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Homo sapiens chromosome 11 clone RP11-281D19 map 11q, WORKING DRAFT
SEQUENCE, 15 unordered pieces.
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                                                                                                                                                                                               Gaps
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Contact: hattoriegsc.riken.go.jp/
Contact: hattoriegsc.riken.go.jp/
Contact: Project Information
Center project name: Humbraftil
Center clone name: RPI1-281D19
Center clone name: RPI1-281D19
Sequencing vector: PCR products; 100% of reads
Sequencing vector: PCR products; 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 170936 bases at least Q30
Consensus quality: 177230 bases at least Q30
Consensus quality: 177536 bases at least Q30
Consensus quality: 177555 bases at least Q30
Consensus quality: 177555 bases at least Q30
Consensus quality: 177555 bases at least Q30
Consensus quality: 177536 bases at least Q30
Consensus quality: 177537 bases; sun-of-contigs
Quality coverage: 5.43x in Q20 bases; sum-of-contigs
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                                                                                                                        Query Match 62.7%; Score 23.2; DB 2;
Best Local Similarity 77.8%; Pred. No. 81;
Matches 28; Conservative 0; Mismatches 8;
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Homo sapiens DNA, clone:RP11-281D19.
Homo sapiens
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54312 contig of
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91654 contig of
1106526 contig of
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31506. 54312
/note="assembly_fragment clone_end:SP6 vector_side:left"
                                                                                                                                                                                                                                                                                  Sequence updated (25ch May-2000).

* NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
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/chromosome="11"
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                                                                                                                                                                   Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, 7x 77030, USA on Dec 20, 2001 this sequence version replaced gi:15624160.

Center: Baylor College of Medicine Center Center EMPLOY COLLEGE CENTER CENTER COMES COMES COMES COMES COMES COMES COMES
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Unpublished
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Consensus quality: 116155 bases at least Q30
Consensus quality: 122636 bases at least Q20
Estimated insert size: 93674; sum-of-contigs estimation
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Center clone name: CH230-3123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     During sequence version replaced gi:13396434.

On Apr 14, 2001 this sequence version replaced gi:13396434.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality)=30; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Puther information can be found at http://www.sanger.ac.uk/HGP/Chr9

RPI1-56D6 is from the library RCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                          AL162426 163338 bp DNA linear PRI 13-APR-2001
Human DNA sequence from clone RP11-56D16 on chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is the entire insert of clone RPI1-56D16 The true left end of clone RPI1-228B15 is at 118147 in this sequence. The true right end of clone RPI1-373J8 is at 71520 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (13-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                       Length 128481;
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                    length
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unknown length
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length
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Pred. No. 1.4e+02;
); Mismatches 9;
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of 1005
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                                                             of 1429
                                           unknown
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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137, .315
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Mammalia; Eutheria; Primates;
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contig
gap of
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/clone="RP11-56D16"
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                                        gap of contig
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Kimberley, A.
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112405:
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113510:
113610:
                                                                                                                                                                   61.18;
75.78;
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Best Local Similarity
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TITLE
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KEYWORDS
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879. .1025
/note="LIMC4 repeat: matches 7501. .7658 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anote="Alusx repeat: matches 3. .312 of consensus" 4137. .4426
Anote="Alusx repeat: matches 1. .296 of consensus" 430. .4539
Anote="LiM4 repeat: matches 3057. .3164 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8459. .8509
/note="MRR69 repeat: matches 2458. .2508 of consensus"
8698. .8725
/note="MRR69A repeat: matches 104. .130 of consensus"
8726. .9030
/note="Aluxx repeat: matches 1, .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1540. 4832

//note-"Aluy repeat: matches 1. .305 of consensus"

1833. 493.

Note-"LIM4 repeat: matches 2957. .3057 of consensus"
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700te-"Alusx repeat: matches 1. .309 of consensus"

9922. .10227

700te-"Alu3o repeat: matches 13. .307 of consensus"

10251. .10561
                                      610. 745 ... Anote-"Alusx repeat: matches 1. .137 of consensus" 746. e689 ... Aluso repeat: matches 1. .136 of consensus"
                                                                                                                                                                                                      .2747 of consensus"
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                                                                                                                                                                            /note="MER20 repeat: matches 2. .215 of consensus" 1247. .1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4941. .5251
/note="AluSg repeat: matches 1. .310 of consensus"
5500. .5803
/note="AluSx repeat: matches 1. .304 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6591. 6893 ... force-"Alug repeat: matches 1. .299 of consensus" 6894. ... 213. ... rocte-"AluJo repeat: matches 1. .296 of consensus" rocte-"AluJo repeat: matches 1. .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293. .9597
note="AluSx repeat: matches 1. .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .311 of consensus"
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Moote—"Alusp repeat: matches 1. 294 of consensus
8085. 8172
Moote—"MIR repeat: matches 35. 134 of consensus"
                                                                                                                                                                                                                                                                                                                                            2147. .2389
//note="WIR repeat: matches 5. .262 of consensus"
2606. .2695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407. .8466
note="AluJ/FLAM repeat: matches 11. .71 of
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                                                                                                                                                                                                                                                                                                                                                                                       2606. .2695 - rewer matches 5. .262 of co
/note="45 copies 2 mer gg 67% conserved"
2907. .3196
                                                                                                                                                                                                                                                                                                                                                                                                                                                        907. 3196
note="AluSc repeat: matches 1. 294 of 6825. 4134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   copies 2 mer gg 62% conserved"
                     .299 of
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note="MER69A repeat: matches 63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L2 repeat: matches 2641.
10811. .10848
116. .609
'note="AluSq repeat: matches 1.
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| 15960. | 15960. | 15960. | 15960. | 15960. | 15960. | 15960. | 15974. | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 16005 | 1600
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/note="AluSx repeat: matches 1. .310 of consensus" 19072. .19102
/note="AluSx repeat: matches 105, .135 of consensus" 19104. .19416
                                                                11145. 11380
/hote="LlME3 repeat: matches 5884. .6122 of consensus"
11565. 11727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13799. 13885

/note="Alusc repeat: matches 47. .298 of consensus"

/note="Alusc repeat: matches 222. .308 of consensus"

/note="75LRNA repeat: matches 236. .317 of consensus"

14066. 14138

/note="repeat: matches 2161. .2240 of consensus"

14163. .14310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MIR repeat: matches 38. .204 of consensus" 1439. .14630
/note="AluJo repeat: matches 1. .282 of consensus" 14671. .14852
/note="Logat: matches 2551. .2743 of consensus" 14965. .15097
/note="FLAMC repeat: matches 1. .133 of consensus" 1517 .15325
/note="MIR repeat: matches 1. .343 of consensus" 15432 .15432 repeat: matches 193. .394 of consensus" 15432
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/note="Alusb repeat: matches 1. 311 of consensus" 20477. 20516
/note="MERAB repeat: matches 500. 540 of consensus" 20541. 20840
/note="Alusx repeat: matches 1. 301 of consensus" 2154. 22344
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15486. 15659
/note="AluJo repeat: matches 123. 299 of consensus"
15660. 15968
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18605. .18762
                                                                                                                                                                                                                                                                                                                 /note="AluSc repeat: matches 1. .309 of consensus" 12362. .12677 /note="L2 repeat: matches 2342. .2681 of consensus" 13235. .13530 /note="AluSc repeat: matches 1. .295 of consensus" 13531. .13782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2743 of consensus"
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                                 .296 of consensus"
                                                                                                                                                                         /note="FAM repeat: matches 1. .163 of consensus"
11728. .11805
/note="39 copies 2 mer ta 93% conserved"
11868. .12182
                                 note="AluSp repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
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Dipublished

Silven, Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Bairen, B., Linton, L., Barna, M., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dadrellano, K., Depyre, E., Devon, K., Dewar, K., Dewar, K., Opoelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Marquis, N., McEanghlin, W., Marquis, N., McEanghlin, J., Marquis, N., McEanghlin, J., Marquis, N., McEanghlin, J., Marquis, N., McEanghlin, J., Molla, M., Morris, W., McCernan, K., McLaughlin, J., Maylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Direct Submission

Lincer Submission

Submitted (199-APR-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jun 25, 2000 this sequence version replaced gi:7342096.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                         AC007430 172588 bp DNA linear HTG 07-DEC-2001
Homo sapiens chromosome 9 clone RP11-94E8 map 9, *** SEQUENCING IN
PROGRESS ***, 7 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 172588)
Birren, B., Linton, L., Nusbeum, C. and Lander, E.
Homo sapiens chromosome 9, clone RP11-94E8
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                                                        Gaps
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Length 163338;
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                                                                                                                                                                                                                                                                                                                                                                                        AC007430.18 GI:8705107
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN
                                                                                                                                 Db 21486 CTGTGTTCACCCAATCCCCTCCTCCTAGGC 21450
  Score 22.6; DB 9;
Pred. No. 1.3e+02;
                                                                                                    1 ctatatccacccatatccccttccccttgcgtgtggg 37
                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center clone name: 94_E_8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR
  61.1%;
75.7%;
Query Match
Best Local Similarity 75.7
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                RESULT 14
AC007430/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
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TITLE
JOURNAL
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133292
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JOURNAL
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Naturo, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Adisbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Blumage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bureat, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, C., Darter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, C., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., David, R., Davila, M.L., Davis, C., David, R., David, R., David, R., Davis, C., David, R., David, R., David, R., Davis, C., Coyle, M.D., Ding, Y., Dinh, H.H., Douthwaite, R.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Ferraguto, D., Flagy, N., Ford, J., Falls, T., Ferraguto, D., Flagy, N., Ford, J., Garza, N., Gill, R., Gabisl, A., Gao, J., Garcia, A., Garner, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hennandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsl, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jud, Y., Joudah, S., Karlsson, E., Jak, Y., Johnson, R., Jolivet, S., Lous, R., Luna, R., Luls, J., Lul, J., Lul, J., Luly, J., Luly, J., Luly, J., Luly, J., Luly, J., Luly, J., Martinez, E., Massey, E., Mawhiney, E., Martinge, B., Martinez, E., Massey, E., Mawhiney, E., Mitchell, T., Morria, S., Martinez, E., Massey, E., Mawhiney, E., Mitchell, T., Morria, S., Martinez, E., Massey, E., Mawhiney, E., Mitchell, T., Morria, S., Martinez, E., Massey, E., Mawhiney, E., Mitchell, T., Morria, S., Martinez, E., Massey, E., Mawhiney, E., Mitchell, T., Morria, S., Martinez, E., Massey, E., Mayer, J., Marting, E., Mitchell, D., Mayer, D., Marting, E., Martinez, E., Massey, E., Mawhiney, E., Mitchell, F., Martin, E., Martinez, E., Massey, E., Martin, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236135 bp DNA linear HTG 20-DEC-2001
Rattus norvegicus clone CH230-3B9, *** SEQUENCING IN PROGRESS ***,
AC093959
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 172588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601 others
                                                      122649 122748; gap of 100 bp
122749 125082; contig of 2334 bp in length
125083 125182; gap of 100 bp
125183 172588; contig of 47406 bp in length.
Location/Qualifiers
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120052 120151: gap of 100 bp
120152 122648: contig of 2497 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RPCI-11 Human Male BAC"
43766 c 42666 g 43574 t 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 22.6; DB 2;
Pred. No. 1.3e+02;
0; Mismatches 9;
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                                                                                                                                                                                                                                      1. .172588
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RP11-94E8"
                                                                                                                                                                                                                                                                                                                                                      /chromosome="9"
/map="9"
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75.78;
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Best Local Similarity 75.7
Matches 28; Conservative
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Rattus norvegicus
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
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KEYWORDS
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Tang, H., Tansey, J., Taylor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmanl, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Walli, R., Wang, S., Warren, R., Washington, C., Watlington, S., Williamson, A., Wilczy, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence It currently consists of 51 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                    Submitted (13-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA
On Dec 20. 2001 this sequence version replaced g1:15627002.

Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      findPhrapList
Consensus quality: 200925 bases at least Q40
Consensus quality: 210235 bases at least Q30
Consensus quality: 217064 bases at least Q20
Estimated insert size: 217481; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 2.9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: Phrap; version 0.990329First call to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21130: contig of 21130 bp in length 21230: gap of unknown length 39576: contig of 18346 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown length
of 13164 bp in length
unknown length
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of 7943 bp in length
unknown length
of 6348 bp in length
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of 5926 bp in length
unknown length
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of 3936 bp in length
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of 8950 bp in length
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of 9051 bp in length
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of 8152 bp in length
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bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                   Unpublished
2 (bases 1 to 236135)
Worley, K.C.
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Location/Qualifiers

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T88687 yd31a01.s1 AA973752 oq16a06.s AA719824 zh39d01.s BB771315 BB771315

Perfect score: Sequence: Scoring table:

OM nucleic

Run on:

Minimum DB Maximum DB

Database

Searched:

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                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                         Trace considered overall poor quality Seq primer: custom primer used High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                      ALIGNMENTS
                     T88687
AA973752
AA719824
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BG025725
R37656
BE757143
AI760326
AI207178
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house mouse.
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KEYWORDS
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                                                                                                        A1786367 uj54d05.x
AU51810 AU151810
AA811417 Ob82h01.s
BE142441 RC2-HT014
B1014164 PM3-ET020
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B1063933 IL3-UT011
BE260926 601153879
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(without alignments)
126.357 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                        Description
                                                                                                             27472414
                                                                      ctatttcccacccatatccccttgggcccttgggtgtggg
     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                  13736207 seqs, 6748477542 residues
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BE142441
BIO14164
BIO774850
BM453604
BIO63933
                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                 IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                        US-09-721-543A-15
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465
606
753
929
281
1064
369
441
464
489
629
616
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R25470 BE490643 BE444887 BE516924

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44 100 110 110 110 110 110 110 110

Score

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Result

24.2 24 23.4

BG607929 BE585665 BG341375

FEATURES

BG677396 602625216 291019 F. rubripes A1139307 9024405.x A1886176 wz63011.x AL522402 AL522402 BE562837 60156557 AW356990 39718 WAR

AQ116520 HS_3000_A AL513845 AL513845 AW469108 Hc77c07.x AG075780 Pan trogl A1765716 wi83f06.x

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                     AA811417 1754 bp mRNA 11near EST 19-FEB-1998 ob82h01.81 NCI_CGAP_GCB1 Homo sapitens cDNA clone IMAGE:1337905 3' similar to TR:O00562 000562 HOMOLOGUE OF DROSPHILA RETINAL DEGENERATION B GENE. ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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Bukaryota.

Bukaryota.

Bukaryota.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 754)

NCI-GGAP http://www.ncbl.nhm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
              9; Length 528;
                                                                             6; Indels
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Location/Qualifiers
DB 6
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Pred. No. 99;
0; Mismatches
                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA811417.1 GI:2881028
          60.0%;
81.8%;
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Unpublished (1997)
                                                                             Conservative
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       Query Match
Best Local Similarity
Matches 27; Conserv
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                                                                                                                                                                                                            g
                                                               /note-"Organ: liver; vector: pwE185-FL3; Site_l: DraIII
/note-"Organ: liver; vector: pwE185-FL3; Site_l: DraIII
(CACCTGTGTC); Site_2: DraIII (CACCATGTC); lst strand cDNA
was primed with an oligo(dT) primer stranded cDNA was
[ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTACTGC], digested
and cloned into distinct DraIII sites of the pwE188-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTC). XnoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <-1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGAAGCACA.

55 a 86 c 88 9
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliai Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 528)

Sota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Samantsu,A., Ozawa,M., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.)

HRI human cDNA project (Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Ozawa,M., Nakamura,Y., Nagai,T., Sugano,S., Isogai,T.)

AL, Nagai,T., Sugano,S., Isogai,T.)

Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel. 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix Research Institute, cDNA library construction: Department of Virology, Institute of Modical Science, University of Tokyo, and Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU151810 NT2RP2 Homo sapiens cDNA clone NT2RP2006151 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NT2RP2006151"
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160 c 164 9 102 t 11 others
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Query Match 58.5%; Score 23.4; DB 9; Length 754; Best Local Similarity 81.8%; Pred. No. 1.7e+02; Matches 27; Conservative 0; Mismatches 6; Indels
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RESULT 4 BE142441/c LOCUS

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DEFINITION

ACCESSION KEYWORDS SOURCE

VERSION

ORGANISM

REFERENCE AUTHORS

MEDLINE COMMENT

JOURNAL

TITLE

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// Site_l: Smal; A mini-library was made by cloning products
// Site_l: Smal;
//
                                   Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 465)
Dias Neto,E., Garcia Corree,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Coldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 09-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: +55-11-2707001
Email: asingpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&t2=PM3-ET0207-090201-008-f04&t3=2001-02-09&t4=1)
Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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601278222F1 NIH_MGC_39 Homo sapiens CDNA clone IMAGE:3610492 5',
BE531296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed agenence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Pred. No. 2.2e+02;
0; Mismatches 10
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High quality sequence stop: 465.
Location/Qualifiers
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Best Local Similarity 74.4%;
Matches 29; Conservative
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 378)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstealn,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: +55-11-2707001
Email: satimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC2-HT0148-071
099-013-f01&t3=1999-10-07&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                           BE142441 378 bp mRNA linear EST 21-JUN-2000 RC2-HT0148-071099-013-f01 HT0148 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 2.1e+02;
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High quality sequence stop: 378.
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BASE COUNT ORIGIN

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/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
/olone="IMAGE:301492"
/clone="IMAGE:301492"
/clone="Lib="NIH_MGC_39"
/tissue_type="adenocarcinoma"
/tab_host="bill08 (phage-resistant)"
/orde="Organ: pancreas; Vector: pOTB); Site_1: Xhol;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIX/hol; Site_1: Xhol;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIX/hol sites using the following 5, adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life
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MIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                  CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: Plate: LLCM266 row: k column: 05
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http://image.llnl.gov
Plate: LLCM1612 row: g column: 12
High quality sequence stop: 435.
Location/Qualifiers
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/clone=Ihb="NIH_MGC=40"
/tissue_type="carcinoma, cell line"
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Pred. No. 2.3e+02;
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Location/Qualifiers
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Email: cgapbs-r@mail.nih
Tissue Procurement: ATCC
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Matches 29; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
E 1 (basses 1 to 929)
NIH-MCC http://mgc.ncl.nih.gov/.
National Institutes of Health, Nammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ArCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution Information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
Plate: LLAM.Zll7 row: o column: 20
High quality sequence start: 180
High quality sequence start: 180
Location/Qualifiers
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoNI; cDNA made by oligo-dT priming.
Directionally cloned into EcoNI/XhoI sites using the following s' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/lab.host="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="bloot="blo
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Pred. No. 3.5e+02;
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    .929
    /organism="Homo sapiens"

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/clone="IMAGE:5493739"
/clone_lib="NIH_MGC_67"
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LOCUS

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/clone_lib="NIH_MGC_19"
/clone_lib="NIH_MGC_19"
/clone_lib="NIH_MGC_19"
/tlssue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain, Vector: porB7; Site_1: XhoI; Site_2: EcoRI: cDNA made ly oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NiH_MGC Library."
30 a 345 c 277 g 212 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 369)
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                                   Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.3. Consortium/LLNL at: Image.llnl.gov
Plate: LLCM193 row: n column: 20
High quality sequence stop: 735.
I. 1064
I. 1064
/organism="Hono sapiens"
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1064)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Onpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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IMAGE:132344 5', mRNA sequence.
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Pred. No. 4.2e+02;
0; Mismatches 6;
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4444 Forest Park Parkway, Box 8501, St. L
eel: 314 286 1800
Fax: 314 286 1810
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Insert Size: 1225
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Best Local Similarity 81.2%;
Matches 26; Conservative
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/organism="Homo sapiens"
/db_xref="texon:9606"
./clone_lib="uT00117"
/dev_stage="Adult"
/dev_stage="Adult"
/fote="Organ: uterus_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A min_ibrary was made by cloning products
Gerived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cubNA amplification were performed under
low stringency conditions."
91 a 53 c 53 g 84 t
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BE260926
BE260926.1 GI:9132626
EST.
                                                                                                         BIO63933
LL3-UT0117-060401-536-B07 UT0117 Homo sapiens CDNA, mRNA sequence.
BIO63933
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 281)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This end of the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=Li3st2=Li3-UT0117-'060401-536-B07st3=2001-04-06st4=1)
Seq primer: puc 18 forward
High quality sequence stop: 281.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                                                                                                                                                                             BI063933.1 GI:14471460
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Fax: +55-11-2707001
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/clone="WHE0370_B03_D06"
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                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="CDB:537936"
/db_xref="Tabb:537936"
/db_xref="Tabb:537936"
/db_xref="Tabb:537936"
/clone=lib="Soares placenta Nb2HP"
/clone=lib="Soares placenta obtained at birth (full term)"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (amp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE490643 441 bp mRNA linear EST 31-JUL-2000 WHE0370_B03_D062S Wheat cold-stressed seedling cDNA library Triticum aestivum cDNA clone WHE0370_B03_D06, mRNA sequence.
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1 (bases 1 to 441)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han Seaton,C.L. and Tong,J.C.
Fr.S., Hsia,C.C., Rang,T., Lazo,G.R., Miller,R., Rausch,C.J.,
The structure and function of the expressed portion of the wheat Unpublished (2000)
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US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1225 Std Error: 0.00
Seq primer: M13RPl
High quality sequence stop: 239.
Location/Qualifiers
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Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
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Pred. No. 4.2e+02;
0; Mismatches 8;
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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Best Local Similarity 77.1'
Matches 27: Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae; Friticeae; Triticeae; Tritice
                                                                                                              BE444887
WHE1129_D06_G11ZS Wheat eticlated seedling root normalized cDNA library friticum aestivum cDNA clone WHE1129_D06_G11, mRNA
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/clone_lib="Wheat cold-stressed seedling cDNA library"
/tissue_type="Seedling"
/dev_stage="Five-day old seedling"
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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
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/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
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1larity 77.1%; Pred. No. 4.3e+02;
Conservative 0; Mismatches 8;
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1129_D06_G11"
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Best Local Similarity
Matches 27; Conserv
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/organism="Triticum aestivum"
/cultiva="Brevor (soft, white, winter, common wheat)"
/db_Arsf="Lawon:4565"
/clone="Inb="Wheat ABA-treated embryo cDNA library"
/tissue_type="Seed embryo"
/dev_stage="Mature dormant seeds"
/lab_host="E. coli DH125"
/note="Weetor: pGAb10; Site_1: ECORI; Site_2: XhoI;
Embryos were cut from mature, dormant seeds and imbibed in
25 mcrow ABA (abscisic acid) in 5 mM Mes buffer, pH 5.7,
for 12 hr at 22 C. The tissue, total RNA, and poly(A)
/note="Vector: Lambda Uni-ZAP XR, excised phagemid pbluescript SK; Site_1: ECORI: Site_2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. The CDNA clones were in vivo excised to give pbluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech Univeristy. Normalization protocol used was that of Soares. Plasmid DNA Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE516924 489 bp mRNA linear EST 08-AUG-2000 WHE06622_H09_0182A Wheat ABA-treated embryo cDNA library Triticum aestivum cDNA clone WHE0622_H09_018, mRNA sequence.
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Bukaryota, Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
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Anderson,O.D., Chao,S., Han,P.S., Hsia,C.C., Johnson,R.R, Kang,Y.,
Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L., Tong,J.C., Verhey,S.D. and Walker-Simmons,M.K.
The structure and function of the expressed portion of the wheat genomes - ABA-treated embryo library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Clontech Matchmaker 3' AD primer.
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4.3e+02;
thes 8; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22.2;
Pred. No. 4.
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Matches 27; Conservative
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Fax: 51
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.

1 (bases 1 to 616)
Anderson, O.D., Chao, S., Dubcovsky, J., Echenique, V., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L., The structure and function of the expressed portion of the wheat genomes - Early reproductive apex CDNA library from Triticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
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                                                                                                                                             Plasmid
                                                                                                                                                                                                                                                                                                                                                                                        ö
RNA were prepared by Steven Verhey in M.K. Walker-Simmons's lab (USDA-ARS, Washington State Univ., Pullman, Washington 99164-6420. A cDNA library was made by Clontech using a combination of random and oling primers. Library was plated and archived by Russell Johnson (Colby College, ME/Walker-Simmons' lab). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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/clone_lib="Triticum monococcum early reproductive apex
cDNA library"
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                                                                                                                                                                                                                                                                                                                               Length 489;
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                                                                                                                                                                                                                                                                                                                          ch 55.5%; Score 22.2; DB 10; Il Similarity 77.1%; Pred. No. 4.4e+02; 27; Conservative 0; Mismatches 8;
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/organism~"Triticum monococcum"
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Fax: 5105595818
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Length	Indels
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55.5%;	ative
Similarity	7; Conserv
Query Match Best Local	Matches 2
	Query Match 55.5%; Score 22.2; DB 10; Length 616; Best Local Similarity 77.1%; Pred. No. 4.5e+02;

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Search completed: June 4, 2002, 17:09:09 Job time: 4542 sec

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Sequence 11, No Sequence 1, No Sequence 2, No Sequence 1, No Seque

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US-08-365-486A-II
US-08-826-136-3
US-08-526-136-3
PCT-US92-00282-1
PCT-US92-00282-2
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Sequence 23, Application US/09397992A
Patent No. 6329175
GENERAL INFORMATION:
APPLICANT: CONKIIN, Darrell
APPLICANT: Grant, Francis J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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ilarity 61.1%;
Conservative
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; OTHER INFORMATION: N 1s any
US-09-397-992A-25
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Sequence 24, Appl
Sequence 24, Appl
Sequence 74, Appl
Sequence 74, Appl
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Sequence 2, A
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Sequence 23,
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Sequence 45,
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-376-259-45
US-08-976-259-45
US-08-979-608A-16
US-08-98-913
US-08-65-259-24
US-08-65-259-24
US-08-762-500-24
US-08-991-789A-207
US-08-991-789A-207
US-08-991-789A-207
US-08-91-257-41
US-08-91-257-41
US-08-134-246-8
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US-08-134-246-8
US-08-134-246-8
US-08-134-246-8
US-08-134-246-8
US-08-137-494-38
US-08-297-410-38
US-08-297-410-38
US-08-297-410-38
US-08-455-526-38
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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NAME/KEY: variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 atttcccacccatatccccttgggcccttgggtgtg 38
                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/397,992A
CURRENT FILING DATE: 1999-09-16
PRIOR APPLICATION NUMBER: 60/101,012
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PSELSED for Windows Version 3.0
SSOFTWARE: FSELSED for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20.4;
Pred. No. 12;
Sequence 25, Application US/09397992A; Sequence 25, Application US/09397992A; Patent No. 6329175; GENERAL INFORMATION: APPLICANT: Conklin, Darrell; APPLICANT: Grant, Francis J.; APPLICANT: Rixon, Mark W.; APPLICANT: Kindsvogel, Wayne; TILE OF INVENTION: Interferon-epsilon; FILE REFERENCE: 98-46
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                       DB 4; Length 585;
                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRSISEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/08/979,608A
FILLING DATE: 26-NO. 6355451-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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                                                                                                                   ; Score 19.2; DE; Pred. No. 35; 1; Mismatches
                                                                                                                                                                                                                                                    531 TTTCATAAGCATATGCCCTTGACYCCTTGGATTT 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 48.0%; Score 19.2; D
Best Local Similarity 67.5%; Pred. No. 39;
Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-01N-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTOREY AGENT INFORMATION:
NAME: MYETS, LOUIS
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                            4 tttcccacccatatcccttgggcccttgggtgt 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Coding Sequence LOCATION: 1...651 SEQUENCE DESCRIPTION: SEQ ID NO: 16: US-08-979-608A-16
                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/08979608A Patent No. 6355451 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1208 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 02110-2804
COMPUTER FEADABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS
                                                                                                                   Query Match
Best Local Similarity 70.6%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1inear
               double
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                                   linear
             STRANDEDNESS:
               ; STRANDEDNES;
; TOPOLOGY:
US-08-976-259-45
                                                                                                                                                                                                                                                                                                                      RESULT 4
US-08-979-608A-16
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APPLICANT: Choi, Gil H.
APPLICANT: Choi, Gil H.
APPLICANT: Welch, Rodney A.
TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 2313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6316609
NUMBER OF SEQUENCES: 142
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave, N.W., Suite 600
CITY: Washington
STATE: DC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 60/031,626 AND US 60/061,953
ATORNEY/AGBNT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0740002/EKS/CBM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VERSION 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,259
FILING DATE: Herewith
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Pred. No. 21;
0; Mismatches
APPLICANT: Rixon, Mark W.
APPLICANT: Kindsvogel, Wayne
TILE OF INVENTION: Interferon-epsilon
FILE REFERENCE: 984 46
CURRENT APPLICATION NUMBER: US/09/397, 992A
CURRENT FILING DATE: 1999-09-16
PRIOR APPLICATION NUMBER: 60/101, 012
PRIOR APPLICATION NUMBER: 60/118,578
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: 60/118,578
PRIOR APPLICATION NUMBER: 60/142,766
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 33
SEQ ID NOS: 33
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Patent No. 6316609
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 371-2600
INFORMATION FOR SRQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.0%;
Best Local Similarity 72.2%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
: LOCATION: (779)...(1354)
US-09-397-992A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
US-08-976-259-45/c
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Gaps
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APPLICANT: Landes, Gregory M.
APPLICANT: Landes, Gregory M.
APPLICANT: Darnor Timothy C.
APPLICANT: Connors Timothy D.
APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
APPLICANT: Van Raay, Terence J.
APPLICANT: WINGER, Katherine W.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: One Mountain Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                      APPLICANT: Lal, Preet!
APPLICANT: Lal, Preet!
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
ADDRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STAFE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 TACCCACCCACACCCCCTTGCCCCATTTTGGGTCG 199
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Pred. No. 50;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
US-08-665-259-24/C
; Sequence 24, Application US/08665259
; Patent No. 6028173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFANX: 415-845-4166
                                                                                                                                                                                                                                                                                 COUNTR:

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
  Corley, Neil C.
Guegler, Karl G.
Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 47.5%;
Best Local Similarity 71.4%;
Matches 25; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 1866 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LIBRARY: COLNTUT03
; CLONE: 1340712
US-09-272-796-13
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                                                                                                                                                                  APPLICANT: Bandman, olga
APPLICANT: Bandman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Guegler, Karl G.
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
805 CTGTCTCACACACATCTGCTCCTCAGCACGTCGGTGTGGG 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIDE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 TACCCACCCACACCCCCTTGCCCCATTTTGGGTCG 199
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                                                                                                                                                                                                                                                                                                                                                                                                                 Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BILLINGS, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                     Sequence 13, Application US/08878989
Patent No. 5885803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/09272796
Patent No. 6207148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1866 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.4%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; IMMEDIATE SOURCE:
LIBRARY: COLNTUT03
; CLONE: 1340712
US-08-878-989-13
                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Bandmar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94304
                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: CA
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US-09-272-796-13
                                                               RESULT 5
US-08-878-989-13
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STREET: One Mount
CITY: Framingham
STATE: Massachuse
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APPLICANT: Landes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-762-500-74/C
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APPLICANT: Burn, Timothy C.
APPLICANT: Connors, Timothy C.
APPLICANT: Dackowski, William R.
APPLICANT: Uan Raay, Terence J.
APPLICANT: Van Raay, Terence J.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME NUMBER OF SEQUENCES:
ADDRESSEE: GENEYME CORPORATION
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Pred. No. 59;
0; Mismatches 10; Indels
                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,259
FILING DATE: 17-JUN-1996
CLASSIFICATION: 435
ATYONEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REGISTRATION NUMBER: 37,315
RECIEMANICATION INFORMATION:
TELEPHONE: (508) 872-8400
TELEPACHONE: (508) 872-5415
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 base pairs
TYPE: MICLEL CALLOCKET NUMBER: SEGUENCE CHARACTERISTICS:
LENGTH: 584 base pairs
TYPE: MICLEL CALLOCKET NUMBER: SEGUENCE CHARACTERISTICS:
LENGTH: 584 base pairs
TYPE: MICLEL CALLOCKET NUMBER: SEGUENCE CHARACTERISTICS:
LENGTH: 584 base pairs
TYPE: MICLEL CALLOCKET NUMBER: SEGUENCE CHARACTERISTICS:
LENGTH: 584 base pairs
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COUNTRY: United States of America
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,500
FILLING DATE: 09-DEC-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1571 TATTTCCCACCCTGAACACCTTGGACAGGTGCTTG 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 tatttcccacccatatccccttgggcccttgggtg 36
                     Massachusetts
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: One Mountain Road
CITY: Framingham
STATE: Mases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-762-500-24/c; Sequence 24, Application US/08762500 patent No. 6030806; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 47.5%;
Best Local Similarity 71.4%;
Matches 25; Conservative
                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 09-DEC-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Framingham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION:
US-08-665-259-24
                  STATE: Mi
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PRIOR APPLICATION DATA:

APPLICATION UNDER:
PRIOR APPLICATION
PRIOR SEASON TO APPLICATION
PRIOR TELEBRA:
PRIOR APPLICATION
PRIOR SEASON TO APPLICATION
PRIOR SEASON TO APPLICATION
PRIOR TELEBRA:
PRIOR APPLICATION
PRIOR SEASON TO APPLICATION
PRIOR SERVING SEASON TO APPLICATION
PRIOR SEASON TO APPLICATION
PRIOR PRIOR PRIOR TO APPLICATION
PRIOR PRIOR PRIOR TO APPLICATION
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APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Ralease #1.0, Version #1.30
GURRBY APPLICATION DATA:
APPLICATION NUMBER: US/09/062,431
FILING DATE: 04-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 41, Application US/09227357

Patent No. 6342581

GENERAL INFORMATION:
APPLICANTY: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZ010P1
CURRENT APPLICATION NUMBER: US/09/227,357

CURRENT FILING DATE: 1999-01-08
EARLIER PILING DATE: 1999-01-08
EARLIER FILING DATE: 1999-07-07
EARLIER FILING DATE: 1999-07-07
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFCATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makt, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 207:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.0%; Score 18.8;
76.7%; Pred. No. 42
                             173 CCATTTACCACCCATATCCCATCAGTCACT 144
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                                                                                                                                                                                 Sequence 207, Application US/09062451
Patent No. 6344550
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nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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Matches 23; Conserv
                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                       RESULT 11
US-09-062-451-207/c
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STATE: We
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Frudakis, Tony N.
Smith, John M.
Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.0%; Score 18.8; DB 4; Length 176; 76.7%; Pred. No. 42; 7tive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                               Query Match 47.5%; Score 19; DB 3; Length 6525; Best Local Similarity 71.4%; Pred. No. 60; Matches 25; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 210121.419C3 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2202 TATTTCCCACCTGAACACCTTGGACAGGTGCTTG 2168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 tatttcccacccatatccccttgggcccttgggtg 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 207:
REFERENCE/DOCKET NUMBER: IG5-9.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 872-8400
TELEPHONE: (508) 872-5415
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 6525 base pairs
TYPE: nucleic acid
STANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-991-789A-207/c

Sequence 207, Application US/08991789A

Patent No. 6225054

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 207:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 176 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                             573..5684
                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: 573.
US-08-762-500-74
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GENERAL INFORMATION:
APPLICANT: Wayne, Jay
APPLICANT: Wayne, Jay
APPLICANT: W. Shuang-yong
TITLE OF INVENTION: Wethod For Construction Of Thermus-E. coll Shuttle
TITLE OF INVENTION: Vectors And Identification of Two Thermus Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2921;
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                                                                                                                                                   Sequence 2, Application US/08904032
Patent No. 6004773
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Corley, Net1 C,
TITLE OF INVENTION: EMBRYOGENESIS PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18.8;
Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                    Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 1882 CTGCTTCCCACCCCAAGCCCCTTGGGTTCT 1853
    1 ctatttcccacccatatcccttgggccct 30
                              49 CTCTTCCCCTCCCATTCCCCTCGTGCCAT 20
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FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 8, Application US/09134246B
; Patent No. 6207377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 2921 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 76.7'
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI,ADNOT03
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LIBRARY: BLANCE
TOTAL 1602555
                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: 11ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                       US-08-904-032-2/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE:
US-08-904-032-2
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EARLIER APPLICATION NUMBER: 60/051,919
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,919
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER APPLICATION NUMBER: 60/055,948
EARLIER FILING DATE: 1997-08-18
                                                           R FILING DATE: 1997-07-08

R APPLICATION NUMBER: 60/052,803

R FILING DATE: 1997-07-08

R APPLICATION NUMBER: 60/052,732

R FILING DATE: 1997-07-08

R APPLICATION NUMBER: 60/051,931

R APPLICATION NUMBER: 60/051,931

R R APPLICATION NUMBER: 60/051,932

R R PILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                                                                                                                                R FILING DATE: 1997-07-08

R PRILING DATE: 1997-07-08

R PLING DATE: 1997-07-08

R APPLICATION NUMBER: 60/051,733

R APPLICATION NUMBER: 60/052,733

R FILING DATE: 1997-07-08

R APPLICATION NUMBER: 60/052,795

R APPLICATION NUMBER: 60/051,919

R APPLICATION NUMBER: 60/051,919
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/051,916
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,930
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 60/055,947
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,964
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/056,360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER APPLICATION NUMBER: 60/058,661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,950
FILING DATE: 1997-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,684
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/051,925 ILING DATE: 1997-07-08
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EARLIER FILING DATE: 1997-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-227-357-41
                                          EARLIER A
EARLIER B
EARLIER A
EARLIER F
EARLIER A
EARLIER P
                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER F
EARLIER P
EARLIER F
                                                                                                                                                                                                                          EARLIER I
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DB 4; Length 1158; Indels

47.0%; Score 18.8; D 76.7%; Pred. No. 56; Live 0; Mismatches

Query Match
Best Local Similarity 76.7
Matches 23; Conservative

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US-09-123-651-2/C

Sequence 2, Application US/09123851

Petent No. 5958405

GENERAL INCRAMITION:

GENERAL INCRAMITION:

MUNBER OF SEQUENCES:

ADDRESSEE: INCYTE PAINAMENT OF THE CONTRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STREET: 374 Porter Drive

CITY: Palo Alto

STREET: BAN Compatible

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER IEM COMPATIS:

MEDIUM TYPE: Diskette

COMPUTER IEM COMPATIS:

MEDIUM TYPE: Diskette

COMPUTER IEM COMPATIS:

MEDIUM TYPE: Diskette

COMPUTER IEM COMPATA:

MEDIUM TYPE: Diskette

COMPUTER IEM COMPATA:

APPLICATION NUMBER: US/09/123,851

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/728,520

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/728,520

FILING NATE:

MAME: Billings, Lucy J.

REGISTRATION NUMBER: PF-0136 US

TELEPHONE: 415-85-055

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1346 base pairs

TYPE: nuclaic acid

TYPE: nuclaic acid

TYPE: DIACETARY

INFORMATION TYPE:

LENGTH: TYPE: ONLECTION

THEMEDIATE SOURCE:

THEMED
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Pred. No. 82;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         47.0%; Score 18.8; D 76.7%; Pred. No. 79; iive 0; Mismatches
TITLE OF INVENTION: Replication Origins
FILE REFRENCE: Thermus Shuttle Vector
CURRENT APPLICATION NUMBER: US/09/134,246B
CURRENT FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 8
LENGTH: 11958
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Best Local Similarity 69.4%;
Matches 25; Conservative
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Best Local Similarity 76.77
Matches 23; Conservative
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; ORGANISM: Thermus sp.
US-09-134-246-8
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11958;
0; Gaps 0;
Search completed: June 4, 2002, 17:47:26
Job time: 6599 sec
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Perfect score:

Sequence:

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Scoring table:

Searched:

Database

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AP000056 Homo sapil
AP000171 Homo sapil
AP000171 Homo sapil
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AP001731 Homo sapil
AP001731 Homo sapil
AC024096 Homo sapil
AC1934 Mus muscul
AL611934 Mus muscul
AL611934 Mus muscul
AL61291 Human DNA
G15622 human Sapil
AC096230 Rattus no
AP00717 Homo sapil
AC090279 Homo sapil
AC091852 Homo sapil
AC091889 Homo sapil
AC09189 Homo sapil
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AC08320 Rattus no
AC10573 Homo sapi
AC096321 Rattus no
AC10525 Mus muscu
AL136523 Human DNA
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Submitted (14-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 18A, UW. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Dec 17, 2000 this sequence version replaced gi:11863543.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not, be found in the sequence submission
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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complete sequence.
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AL031726.22 GI:11875952
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TITLE
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw.; SWISSPROT; Tr.; TREMBL; WP: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping http://www.sanger.ac.uk/HGP/ChI Sanger Centre Chromosome 1 Mapping http://www.sanger.ac.uk/HGP/ChI Sanger Centre Chromosome 1 Mapping http://www.sanger.ac.uk/HGP/ChI Sconstructed by the group of http://www.chori.org/bacpac/home.htm

VECTOR: porpac2

IMPORTANT: This sequence is not the entire insert of clone http://www.chori.org/bacpac/home.htm

VECTOR: porpac2

IMPORTANT: This sequence is not the entire insert of clone spections only once, except for a 100 base overlap.

The true left end of clone RP4-800F24 is at 1 in this sequence. The receipt and contains it at 125401 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6388. .6637

/note="MIR repeat: matches 3. .262 of consensus"
7575. .7695

/note="Liz repeat: matches 2623. .2744 of consensus"
10912. .11284

/note="MIRTIAL repeat: matches 20. .365 of consensus"
11990. .12450

/note="LRZ repeat: matches 1. .449 of consensus"
12894. .13515

/note="match: STS: Em:G56281"
12969. .13075

/note="Liz repeat: matches 2575. .2690 of consensus"
13538. .13551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .6153 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-"L1MA4 repeat: matches 4221. .6294 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            603. .5798
note="MLT1F repeat: matches 352. .539 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7792. 3956
706-"L2 repeat: matches 1740. 1897 of consensus" 7419
706-"L2 repeat: matches 2123. 2335 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1636. .4734
/note="L2 repeat: matches 2648. .2749 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5919. .6176 Ante-"MLTIF repeat: matches 10. .252 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3677. 3785
Mote-"MER69A repeat: matches 1. .110 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note-"L2 repeat: matches 2256. .2268 of consensus" 3552. .13868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="AluJo repeat: matches 3. .312 of consensus" 13869. .14262
/note="L2 repeat: matches 2268. .2679 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .249 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .3162
note="LiPA15 repeat: matches 5683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440. .5585
note="MIR repeat: matches 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1403. .4605
/note="MIR repeat: matches 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .125500
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="q23.2-24.3"
/clone="RP5-1018K9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RPCI-5"
1. .2074
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Consensus...

26309. 27011

Ancte-"Link Tepeat: matches 3454. 4224 of consensus...

Ancte-"Link Tepeat: matches 3454. 4224 of consensus...

27012. 27088

Anote-"Link Tepeat: matches 1. 89 of consensus...

27012. 27878

Anote-"Link Tepeat: matches 4216. 4507 of consensus...

27372. 27878

Anote-"Link Tepeat: matches 4771. 5297 of consensus...

Anote-"Link Tepeat: matches 13. 312 of consensus...

Anote-"Alu3b repeat: matches 13. 312 of consensus...

Anote-"MER21B repeat: matches 71. 788 of consensus...

Anote-"MIR repeat: matches 59. .251 of consensus...

Anote-"MIR repeat: matches 13. .261 of consensus...

Anote-"MIR repeat: matches 13. .261 of consensus...

Anote-"Alu3r repeat: matches 13. .301 of consensus...

Anote-"Alu3r repeat: matches 13. .301 of consensus...

Anote-"Alu3r repeat: matches 13. .308 of consensus...

Anote-"Alu3r repeat: matches 13. .288 of consensus...

Anote-"Alu3r repeat: matches 13. .298 of consensus...

Anote-"Alu3r repeat: matches 13. .298 of consensus...
                                                         consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   consensus,
                                                                                                                                                                                                                                                                                                                                                                                                                15232. 15434

/note="7 copies 29 mer 66% conserved"
/note="MIR repeat: matches 75. .260 of consensus"
/note="MIR repeat: matches 25% .210 of consensus"
/note="L2 repeat: matches 25% .2710 of consensus"
/1637. 11733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MSTB repeat: matches 1. .426 of consensus" 19420. .19817 / note="MT1B repeat: matches 6. .390 of consensus" 2.1667 .21667 / note="20 copies 3 mer gag 78% conserved" 2.2077 .22227 / note="MLT1B repeat: matches 359 .504 of consensus / note="MLT1B repeat: matches 359 .504 of consensus / note="MLT1B repeat: matches 359 .504 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32240. 32562 Financial Consensus Anote-Alucx repeat: matches 1. 312 of consensus 33414. 33457 Financial Copies 4 mer acac 88% conserved financial copies 4 mer acac 88% conserved financial copies 4 mer acac 88% conserved financial copies 5 financial financi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .503 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .405 of consensus"
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/note="MLT1-INTERNAL repeat: matches 1019. .1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="AluSg/x repeat: matches 118. .304 of 5993. .26105
                                                   .294 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22323. 22478 copies 2 mer aa 59% conserved" 23525. 24734 chote="Limb repeat: matches -15. 1314 of
                                                                                                                                                                                                             15225. .15432
hore="land-copies 2 mer ct 77% conserved"
1528. .15419
/note="6_copies 32 mer 83% conserved"
/note="AluSg/x repeat: matches 168.
15207. .15430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24737. .25041
/note="AluJo repeat: matches 1.
25100. .25570
/note="MLTID repeat: matches 5.
25807. .25992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note-"LTR7 repeat: matches 1.
                                                         15207. .15430
/note="56 copies 4 mer of 15225. .15432
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Insert size: 164136; sum-of-contigs
Insert size: 165381; 5.5% error; agarose-fp
Quality coverage: 6.98x in Q20 bases; sum-of-contigs Quality
coverage: 7.00x in Q20 bases; agarose-fp
                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 23; DB 2; Length 164736;
Pred. No. 39;
0; Mismatches 10; Indels 0
                                                                                                                                                                                                                                                                                                                                                                            50412 505111: gap of 100 bp 577 bp in length 57889 57188: gap of 100 bp 57889 57188: gap of 100 bp 57189 69975: contig of 5789 bp in length 89877 89976: gap of 100 bp 8997 95765: contig of 5789 bp in length 95866 116678: contig of 20813 bp in length 11679 116778: gap of 100 bp 116779: gap of 100 bp 151648 151747: gap of 100 bp 151648 151747: gap of 100 bp 151748 164736: contig of 12889 bp in length 151748 164736: contig of 12889 bp in length.
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                                                                                                                                                                                                                                                                                                                                                              50411: contig of 50411 bp in length
  Consensus quality: 162752 bases at least Q40 Consensus quality: 163426 bases at least Q30 Consensus quality: 163802 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 57345 TTTATCACACCAATGTCCCTATGGTCCCCTGGCTGTGGG 57383
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/note="assembly_fragment:01774"
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/note="assembly_fragment:01200
fragment_chain:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89977. .95765
/note="assembly_fragment:00719
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116779. 151647
//note="assembly_trugment:01730
fragment_chain:2"
151748. 164736
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fragment_chain:2
clone_end:T7
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hote="assembly_fragment:02233
:ragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57189. .89876
/note="assembly_fragment:00092
fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RP11-233016"
/clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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32591 c 31938 g
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ilarity 74.4%;
Conservative
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Best Local Similarity
Matches 29; Conserv
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
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Homo sapiens chromosome 1 clone RP11-233016, *** SEQUENCING IN
PROCESS ***, 7 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 164736)
Plumb, B.
                                                                                                                                                                                                                                                                   Consensus."

201578. 37683

7016-"MIR repeat: matches 30. 145 of consensus."

37725. 37849

7016-"MIR repeat: matches 20. 144 of consensus."

7016-"MIR repeat: matches 20. 144 of consensus."

7016-"match: 375: Em:G07786."

39197. 39297

7016-"P. Copies 3 mer taa 96% conserved."

39490. 39533

7016-"11 copies 4 mer ggtt 90% conserved."

3954. 39812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 27, 2000 this sequence version replaced gi:9926766.
                                                          //ote="Linel repeat: matches 5601. .6062 of consensus" 35620. .36011
//ote="match: STS: Em:HSPE71D11"
//ote="Lines repeat: matches 6021. .6032 of consensus" 35688. .3603
//ote="Lines repeat: matches 5615. .5755 of consensus" 36837. .36963
//ote="MRR57-internal repeat: matches 7145. .7268 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  consensus
                       .302 of consensus"
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Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; LOB752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40316. .40341

/note="13 copies 2 mer tt 92% conserved"

40785. .40853

/note="LIMD2 repeat: matches 5831. .5897

40877. .40900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10877. .40900
/note="12 copies 2 mer tt 95% conserved"
4914. .35125
note="AluSg/x repeat: matches 97.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_CANCELLED
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Best Local Similarity 74.4
Matches 29; Conservative
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Wartun, D., Adams, C., Adio-Oduola, B., Ali-osman, F. R., Allen, C., Alabrooks S. L., Amacatunge, H. C., Are, J. R., Banks, T., Banks, T., Babrooks S. L., Amacatunge, H. C., Are, J. R., Banks, T., Barbaria, J. Babrooks S. L., Amacatunge, H. C., Are, J. R., Banks, T., Barbaria, J. Banton, S. Britan, R. D., Burkett, C., Burkett, C., Chowdhry, I., Christopoulos, C., Cleveland, C. D., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C. D., Chen, R., Chen, Z., Chowdhry, I., Dinh, H. H., Douthwalte, K. J., Davis, C., Davis, C., Durbin, K. J., Barnett, C. Davis, C., Durbin, K. J., Barnett, C. J., Earnett, C. J., Ferraguco, D., Flagg, N. Ford, J. Davy, Carroll, L., Dedertch, D., Palaney, K. R., Delaney, K. R., Didgaco, O., Davy, Carroll, L., Dedertch, D. A., Delaney, K. R., Deper, H., Carca, R. Carroll, R., Garceia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunaratno, P., Hallon, F. Hamilton, K., Harris, C., Harris, K., Harris, C., Harris, C., Harris, C., Harris, C., Hander, J., Hallyk, S., Hume, J., Jackson, L. E., Jacobson, B., Jaz, Y., Johnson, R., Maheshwart, M., Moser, D., Martinez, R., Martinela, R., Martinez, E., Marsey, E., Martinez, E., Marsey, E., Martinez, E., Marsey, E., Mayen, N., Nickerson, E., Novedo, M., Mattinez, E., Marsey, E., Mayen, N., Nickerson, E., Novedo, M., Perez, L., Perez, L., Peters, R., Wall, R., Syack, A., Rojlad, M., Rojas, A., Rojlad, M., Rojas, A., Rojlad, M., Rojas, A., Rojlad, M., Rojas, A., Rojad, A., Panes, A., Tamer, 
                                                                   AC098752 65064 bp DNA linear HTG 20-DEC-2001
Rattus norvegicus clone CH230-39G3, *** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (01-NOV-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----- Project Information
                                                                                                                                                                                         AC098752.2 GI:17972917
                                                                                                                                12 unordered pieces.
                                                                                                                                                                                                                                                                                          Rattus norvegicus
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                                                                                                                                                                                                                                                             Norway rat.
RESULT 3
AC098752/c
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 42 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Consensus quality: 51113 bases at least Q40
Consensus quality: 54226 bases at least Q30
Consensus quality: 57793 bases at least Q20
Estimated insert size: 29709; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 0.3x in Q20 bases; sum-of-contigs estimation
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; gap of unknown length

; contig of 2706 bp in length

8; gap of unknown length

7; contig of 1939 bp in length
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of 2167 bp in length
unknown length
of 1108 bp in length
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contig of 2811 bp in length
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Sequencing vector: plasmid: LO8752; 100% of reads Chemistry: Dye-terminator Hig Dye: 100% of reads consensus quality: 14952 bases at least Q40 Consensus quality: 152642 bases at least Q30 Consensus quality: 154560 bases at least Q20 Insert size: 156095; sum-of-contigs Insert size: 156095; sum-of-contigs Quality coverage: 4.04x in Q20 bases; sum-of-contigs Quality coverage: 4.03x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently a consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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2691 10620: contig of 7930 bp in length
10621 10720: gap of 100 bp
10721 39969: contig of 29249 bp in length
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87238 99117: contig of 11880 bp in length
99118 99217: gap of 100 bp
99218 112196: contig of 12979 bp in length
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1. 2590
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2691. 10620
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/note="assembly_fragment:00340
fragment_chain:2"
99218 .112196
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fragment_chain:2"
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10721. .39969
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40070. .87137
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fragment_chain:1"
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117084. 121151
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121252. .134800
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/db_xref="taxon:96)6"
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HOMO sapiens chromosome 1 clone RP11-25414, *** SEQUENCING IN
AL355994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (09-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Sep 9, 2000 this sequence version replaced gi:9588227.
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    65064
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    /db_xref="taxon:10116"

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Pred. No. 50;
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------ Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- Summary Statistics
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HTG; HTGS_PHASE1; HTGS_CANCELLED.
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Best Local Similarity 79.4'
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COMMENT

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Submitted (21-DEC-2000) Sandilands A., Blochemistry, School of Life
Sciences, Dow Street, DD4 7AS, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSKRRYADLPSGTNSSMPVQRHRVSSLRGTHSPSSLDSPPASR
TSAVGSLVRAPGVYVGVAPSGGIGGLGARVTRRALGISSVFLQGLRSSGLANVPAPGP
ERDHTTVEDLGGCLVEYMTKVHALEQVSQELETQLRAHLESKAKSSGGWDALRASWAS
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Bfsp2 gene: CP49 protein; intermediate filament protein; phakinin.
house mouse.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                         MMU304861 24180 bp DNA linear ROD 21-DEC-200 Mus musculus partial Bfsp2 gene for phakinin (CP49 protein), exon
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a 41621 c 41264 g 35885 t 1002 others
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illarity 75.7%; Pred. No. 64;
Conservative 0; Mismatches 9;
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/note="assembly_fragment:01275
clone_end:SP6
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Sandliands, A. and Quinlan, R.A.
Squence analysis of the mouse CP49 gene
Unpublished
2 (bases 1 to 24180)
                                                                                                                                                                                                                                                             Db 76307 CTAAATCCCACCCAGCTCCCTGAGGCCCCTGGG 76274
                                                                                                                                                                              Score 22.8; Di
Pred. No. 47;
0; Mismatches
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/protein_id="CAC83162.1"
/db_xref="GI:17977856"
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/organism="Mus musculus"
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/db_xref="taxon:10090"
7537. .8028
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7537, 8028
/gene="Bfsp2"
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7537. .>8028
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79.4%;
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Best Local Similarity 79.4
Matches 27; Conservative
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Best Local Similarity
Matches 28; Conserv
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1. (bases 1 to 19972)

Muzny, D.M., Admarcinge, H.C., Are, J.R., Banks, T., Barbaria, J., Babrooks, S. L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Babrooks, S. L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Burnok, J., Bimage, K., Blanks, M., Brown, M., Brydan, N.P., Burbay, C., Burch, P., Burch, P., Burch, P., Burch, P., Burch, P., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Cavezos, S.R., Chacko, J., Chavez, D., Chen, G., Coyle, M.L., Dadria, C., Ding, Y., Dan, M.L., Davia, M.L., Davia, C., Coyle, M.L., Davia, C., Din, M.L., Davia, M.L., Davia, C., Din, M.L., Davia, Carroll, L., Dodert, C., David, R. J., Ding, M. Ford, J., Dugan-Focha, S., Durbin, M.J., Carla, D., Edara, D., Edara, G., Carcer, H., Burch, M., Calla, C., Ebri, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, N., Gill, R., Gorlet, J., Garler, M., Garner, T., Garza, N., Gill, R., Gorlet, J., Garder, M., Garrer, M., Garza, N., Gill, R., Gorlet, J., Garrer, M., Garrer, M., Garza, N., Garrer, M., Garza, M., Hernandez, J., Hernandez, J., Hernandez, J., Hernandez, J., Hernandez, J., Howard, S., Katlason, E., Mordon, B., Houst, M., Morris, S., Katlason, E., Marchiney, E., Man, U., King, L., Korvah, J., Sakson, E., Lichtarge, O., Lieu, G., Lui, J., Lui, M., Lui, J., Lu
ACU83820 139572 bp DNA linear HTG 24-NOV-2001
Rattus norvegicus clone RP32-290H10, WORKING DRAFT SEQUENCE, 4
unocéared pleces.
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Submitted (01-OCT-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA
On Nov 24, 2001 this sequence version replaced gi:13346542.
Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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Worley, K.C.
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Rattus norvegicus
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AC096321
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KEYWORDS
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                                                           COMMENT
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                                                     Sequencing vector: M13; L00821
Chemistry: Dye-primer Bodipy: 16% of reads
Chemistry: Dye-terminator Big Dye: 84% of reads
Assembly program: Phrap; vecrsion 0.990329
Consensus quality: 138854 bases at least Q40
Consensus quality: 139247 bases at least Q30
Consensus quality: 139299 bases at least Q30
Estimated insert size: 138724; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 11.6x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 58;
0; Mismatches 9;
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Sequencing vector: M13; L08821
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/organism="Rattus norvegicus"
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Center clone name: RP32-290H10
                   -- Summary Statistics
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/clone="RP32-290H10"
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Waterston, R.H.
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Waterston, R.H.
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Waterston, R.H.
Direct Submission
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Matches 28; Conserv
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AC016738/C
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Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J. Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J. Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J. Benton, J., Bingage, K., Blankshoury, R., Bonin, D., Bouck, J., Bowle, S., Bileva, M., Bryant, N.P., Buhay, C., Burch, P., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavaros, S.R., Chacko, J., Chevez, C., Chen, G., Chen, C., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davis, C., Dathorne, S.R., David, R., Davis, M. L., Davis, C., Davis, C., Dann, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Duyan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Esotter, P., Faratis, P., Garis, J., Gareis, A., Garner, T., Forster, P., Faratis, P., Gabis, J.A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hawes, A., Hernandez, J., Hernandez, O., Hadgson, A., Hogtson, M., Holloway, C., Honlins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, E., Jacobson, B., Jackson, A., Hogtson, M., Holloway, C., Lewis, L., Li, J., Li, Li, J., Li, Lu, M., Leal, B., Lewis, L., Li, J., Li, Lu, M., Liu, K., Lewis, L., Li, J., Li, Lu, M., Liu, K., Martindale, A., Martinez, E., Mawkiney, E., Matchell, T., Mohabbat, R., Morgen, M., Mortis, S., Matchin, N., Nguyen, N., Nickerson, E., Nwetson, N., Nickerson, S., Nuckenkwo, S., Nuckerson, S., Sankerson, S., Sankerson, S., Sankerson, S., Sankerson, S., Sankerson, S., Sankerso
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Submitted (01-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MAD 63108, USA
On Feb 1, 2002 this sequence version replaced gi:17933871.
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Mammalia; Eutheria; Rodentiu; Sciurognathi; Muridae; Murinae;
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Center code: WUGSC
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42570 c '40978 g 48397

    . .183289
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Best Local Similarity 75.7'
Matches 28; Conservative
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Rattus norvegicus
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TITLE

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Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Perez, J., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Ponte, M., Ruiz, S., Sacry, G., Scherer, S., Soctt, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Tansey, J., Taylor, T., Tabor, P., Tamerisa, R., Tamerisa, R., Tang, H., Tansey, J., Taylor, T., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Walliams, G., Williamson, A., Wleczyk, R., Wooden, S., Weinstock, G. and Gibbs, R., Tang, W., C., Wu, Y., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/doss/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pleces as not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Worley, K.C.
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced g1:17062233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 215824 bases at least Q40
Consensus quality: 218558 bases at least Q30
Consensus quality: 220420 bases at least Q30
Estimated insert size: 219320; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: 4.9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: Phrap; version 0.990329First call to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of 25738 bp in length gap of unknown length contig of 21457 bp in length gap of unknown length contig of 22923 bp in length gap of unknown length
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49061: gap of unknown length
81934: contig of 32873 bp in length
82034: gap of unknown length
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of 15443 bp in length
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of 11029 bp in length
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of 8653 bp in length
unknown length
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: hgschelp@bcm.tmc.edu
------ project information
Center project name: GEXR
Center clone name: CH230-173F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Summary Statistics
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Nativas.

(bases 1 to 67560)

Nuzny, D.M., Adams, C., Adlo-Oduola, B., All-Osman, F.R., Allen, C., Adams, C., Adlo-Oduola, B., All-Osman, F.R., Allen, C., Carron, T.E., Benton, J., Burkett, C., Burkell, R.L., Bryant, N.P., Buhay, C., Burkett, C., Burkell, R.L., Bryant, N.P., Buhay, C., Carton, T.E., Carton, C., Chen, R., Chowdry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M., D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., David, C., David, C., Davis, C., David, C., Carca, C., Harris, C., Harris, C., Garca, C., Garca, C., Harris, C., Harris, C., Huber, J., Huber, J., Huber, J., Humas, J., Homas, L.F., Homas, L.F., Homas, L. L., Lid, C., Lid, J., Lid, C., Lid, J., Lid, C., Li
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*** SEQUENCING IN PROGRESS ***,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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53279 c 51198 g 58878 t 1413 others
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224294: contig of 1898 bp in length 224394: gap of unknown length 226559: contig of 2165 bp in length 226659: gap of unknown length 228123: contig of 1464 bp in length.
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                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/chromosome="Rf1"
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75.7%; Pred. No. 56;
Live 0; Mismatches
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1. .228123
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HTG; HTGS_PHASE1.
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Best Local Similarity
Matches 28; Conserv
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Mus musculus clone RP24-133K20, LOW-PASS SEQUENCE SAMPLING.
AC102525
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HTG: HTGS_PHASE0.
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Subaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 70165)
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/db_xref="taxon:10116"
/clone="CH230-8P8"
i 12041 c 11986 g 19717 t
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unknown of 1481 h
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72.5%; Pred. No. 73;
ive 0; Mismatches
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Best Local Similarity 72.5
Matches 29; Conservative
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NOTE: This is a 'working draft' sequence. It currently consists of 38 contigs. The true order of the pieces is a sequence frown and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Consensus quality: 54982 bases at least Q40
Consensus quality: 59759 bases at least Q30
Consensus quality: 63487 bases at least Q20
Estimated insert size: 48793; sum-of-contigs estimation
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Direct Submission
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Web site: http://www-seq.wi.mit.edu
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                                                                                      Unpublished
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TITLE JOURNAL

COMMENT

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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw: SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP: Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human thtp://www.sanger.ac.uk/HGF/Chr13

RPI1-103K9 is from the library RPC1-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.chori.org/bacpec/home.htm
VBCTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
RRD1-103K9 It may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true left end of clone RP11-431022 is at 84860 in this
sequence. The true right end of clone RP11-209319 is at 2000 in
this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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/note="Sequence from uni-directional dGTP big dye terminator reads only."
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/note="match: STS: Em:HSPH11F3"
complement(19452..19963)
/note="match: STS: Em:G63496"
45385..45406
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/clone="RP11-103K9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib-"RPCI-11.1"
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Best Local Similarity 72.5%;
Matches 29; Conservative
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SOURCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission

Submitted (23-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
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                                                                                                                                                                                                                                                                                                                                                                                                           11823: gap of 4 100 bp 4255: contig of 702 bp in length 42300: contig of 6702 bp in length 13400: gap of 100 bp 100 bp 44101: contig of 675 bp in length 44201: gap of 100 bp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9763: gap of 100 bp 50442: contig of 679 bp in length 0542: gap of 100 bp 12123: contig of 693 bp in length 1335: gap of 100 bp 52022: contig of 687 bp in length 1212: gap of 100 bp
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                                                                                                                                                                                                                                    in length
                                                                                                                                                                                                                                                                                                 reconting of 702 bp in length ap of 100 bp in length conting of 696 bp in length
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contig of 686 bp in length
ap of 100 bp
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6
                                             4 37813: gap of 100 bp

4 3821: contig of 708 bp in

2 3821: ontig of 702 bp in

3 39323: contig of 702 bp in

4 39423: gap of 100 bp

4 40125: contig of 702 bp in

6 40225: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 bp
of 682 bp
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 tatttcccacccatatccccttgggcccttggg 34
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               contig of
                                                                                                                                                                                                                                                                                                                                                                                                                   41823: gap of
42525: contig
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53608: contig
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                                                                                                                                                                                                                                                                                                                                              gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:15384799
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78.8%;
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                                                                                                                                                                                                                                                                                                        40927
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Best Local Similarity 78.8
Matches 26; Conservative
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EUKATYOLA: Betazoa: Chordata: Craniata; Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates: Catarrhini: Hominidae; Homo. 100000)

EL (bases 1 to 100000)

RE Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
Homo sapiens 890,291bp genomic DNA of 21q22.1 (RECION: D21S226-AML CLONE RANGE: B2344Fl4 f50E9)

Published Only in Database (1999) in press

E (bases 1 to 100000)

Re Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.

Direct Submission

NL Ender Committed (10-MAY-1999) to the DDBJ/EMBL/GenBank databases.

Masabira Hattori, The Institute of Physical and Chemical Research (RIKEN). Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1

Kitasaro, Sagamihara, Kanagawa 228-8855, Japan

(E-mail: hattori@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-42-778-9923, Fax: 81-42-778-9924)

E. coli transposon sequences which integrated in the original/previous sequences which integrated in the original/previous sequences which integrated in the original/previous sequences experimentally, removed the insertion sequences. Teconstituted the present data. The sequencing project is supported by Japan Science Technology Corporation (JST) and The Insertion and The Insertiuc of Physical and Chemical Research (RIKEN).
sakaki@hgc.ims.u-tokyo.ac.jp
Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D. The
sequence is submitted by Human Genome Sequencing in ALIS project of
JST.
                                                                                                                     Japan Science and Technology Corporation (JST) 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081 Japan For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/) or send email to webmaster@www.alis.tokyo.jst.go.jp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /standard_name="D21S65"
/note="D21S65.PCR1;The location is between each flanking
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/map="21922.1"
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/db_xref="taxon:9606"
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/db_xref="GDB:191986"
a 22172 c 22427 g 28
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Best Local Similarity 72.5
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                 Laboratory as a JST sequencing team.
Principal Investigator: Yoshiyuki Sakaki Ph.D.
Phone: +81-3-5449-5622, Fax: +81-3-5449-5445,
sakakiehgc.lms.u-tokyo.ac.jp
Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D. The
JST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Japan Science and Technology Corporation (JST)
5-3. Yonbancho, Chiyoda-ku, Tokyo 102-0028 Japan
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top. html)
or send email to webmaster@www-alis.tokyo.jst.go.jp/HGS/top. html)
Location/Qualifiers
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                                                                                                                                                                                 JST
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens 817,199bp genomic DNA of 21q22.1 GART and AML region
Published Only in DataBase (1999) In press
C (bases 1 to 100000)
                                                                                                                                                                         Masahira Hattori, Kitasato University, Department of Science, JSJ Sequencing Laboratory; Kitasato 1.15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)
This sequence is conducted by Kitasato University JST sequencing
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Principal Investigator:Yoshiyuki Sakaki Ph.D.
Phone: +81-3-5449-5622, Fax : +81-3-5449-5445,
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                Homo sapiens genomic DNA, chromosome 21q
Published Only in DataBase (1998) In press
2 (bases 1 to 100000)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Direct Submission
Submitted (11-MAY-1998) to the DDBJ/EMBL/GenBank databases.
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Homo sapiens genomic DNA of 21q22.1, GART and AML related,
SLC5A3-f4A4 region, segment 7/8, complete sequence.
AP000124
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22366 c 22356 g 28618
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
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Matches 29; Conserv
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Direct Submission

Direct Submission

Equests: clonerequestesdeanger.ac.uk

On Jun 20, 2000 this sequence version replaced gi:8573762.

On Jun 20, 2000 this sequence version replaced gi:8573762.

On Jun 20, 2000 this sequence version replaced gi:8573762.

During sequence assembly data is compared from overlapping clones, where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: Sw: SWISSPROT: Tr: TREMBL: WP: WORMPEP: Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence chromosome 20, constructed by the Sanger Centre Chromosome 20 http://www.sanger.ac.uk/HGP/Chr20

MAPPING Group Further information can be found at http://www.sanger.ac.uk/HGP/Chr20

IMPORTANT: This sequence is not the entire insert of clone RP4-530151 in may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true right end of clone RP4-530115 is at 111039 in this sequence. The true right end of clone RP6-8941K is at 101 in his sequence. The true right end of clone RP6-8941K is at 101 in this sequence. The true right end of clone RP6-8941K is at 101 in this sequence. The sequence was finished as follows unless otherwise noted all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequenced by at least one plasmid subclone; and the assembly was confirmed by restriction digest.

RP4-53015 if is from the library RPCI-4 constructed by the group of pieter deline assembly was confirmed subclone; and the assembly was confirme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human DNA sequence from clone RP4-530115 on chromosome 20 Contains the 3' end of the PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1 (EC 3.1.3.48), the gene for a novel protein similar to placental protein DIFF40, an RP136 (60S ribosomal protein L36) pseudogene, a novel gene, two putative novel genes, AL133230
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL133230.25 GI:8574103
HTG; DIFF40; protein tyrosine phosphatase; PTPN1; ribosomal
protein; RPL36.
                                                                                                                                                                                                 Length 100000;
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                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                   Db 61873 CCATTGCCTTCGCATATACAGTTGGGCCCTTGAATGTTGG 61834
                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                              1 ctatttcccacccatatccccttgggcccttgggtgtggg 40
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VECTOR: pCYPAC2.
/chromosome="21"
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26981 a 22407 c 22383 g 28229 t
                                                                                                                                                                                          56.0%; Score 22.4; Di
72.5%; Pred. No. 71;
:ive 0; Mismatches
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Wall,M.
                                                                                                                                                                                             Query Match
Best Local Similarity 72.5'
Matches 29; Conservative
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                                                                   BASE COUNT
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
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Location/Qualifiers 1. .111039

FEATURES

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c 13108. 13577

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on 13974. 13997

/note="la copies 2 mer tc 100% conserved"

a 14859. 15356

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join (<20252. 21042, 24558. 24658, 27969. 28067, 34106. 34243, 38009. 38218, 38757. 38918, 39292. 39515, 40854. 41049, 42281. 44351]
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match: ESTS: Em:AM31962 Em:M33689 Em:M31724
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Em:A1700791 Em:A1802004 Em:A1468393 Em:A10403863
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DLEPPPEHIPPPRPRPRRILEPHNGKCREFFPNHQWVKEETQEDKDCPIKEEKGSPLN
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                                                                                                                                                                               / Journ - Trini
/ Journ - Trini
29085. 29126
/ Anote - 3 copies 14 mer 97% conserved | 29101. 29289
/ Anote - 7 copies 27 mer 88% conserved | 29209. 29250
/ Anote - 3 copies 14 mer 97% conserved | 29237. 29775
/ Anote - 3 copies 13 mer 92% conserved | 29304. 29345
/ Anote - 3 copies 14 mer 90% conserved | 29304. 29345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29372. .29413
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30667. 30759
/note="3 copies 31 mer 78% conserved"
31563. .31618
/note="2 copies 28 mer 94% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29319. .29399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(40239. .40772)
7.00te-match: GSS: Em:AQ482949"
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Length 111039;

56.0%; Score 22.4; DB 9;

Query Match

OM nucleic

Run on:

Sequence:

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TA297H02Q 5:4 bp DNA linear GSS 13-DEC-2000 T. brucei sheared genomic ENA clone 297h02, reverse sequence, genomic survey sequence.
AL489616 I GI:11864911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Constructed at the Institute for Genomic Research (TIGR),
Constructed at the Institute for Genomic Research (TIGR),
Constructed at the Institute for Genomic Public From a cloned population of
Rockville, MD. Genomic DNA isolated from a cloned population of
trypanosoma brucei (TRE0927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v +1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trypanosoma.

1 (bases I to 534)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         barrers, value sets and sets are an all able small in the sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualiflers
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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BM331631

BM631631

AL670159

AL670141

AL677141

AL15465

BF896828

W66814

AQ72254

AA125134

AA125134

AA125134

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BBA253888

BBA253888
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BI542879
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BM335923
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AI714407
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BP987540 MR3-GN015
AG112675 Pan trog1
BF813535 IL5-C1014
AZ056792 ZM0161P17
BI338782 434533 MA
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BI388746 949045A07
AW091238 683027B06
                                                                  4, 2002, 17:08:55 ; Search time 4272.65 Seconds (without alignments) 126.357 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                     27472414
                                                                                                                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                               13736207 seqs, 6748477542 residues
                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                 - nucleic search, using sw model
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Minimum DB & Maximum DB &

Database

/organism="Trypanosoma brucei"

source

FEATURES

/strain="TREU927"
/db_xref="taxon:5691"
/clone="297h02"
117 c 135 g

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BASE COUNT

AW917931 BI388746 AW091238

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AI586386 AI920579 AI438418 A1600794 A1065660

AI629579

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Query Match
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BF987540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=MR3&t2=MR3-GN0150-101000-001-bl2&t3=2000-10-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 24
High quality sequence stop: 217
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 217)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Concer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
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               Length 534;
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20202663
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0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="cay0150"
/dev_stage="Adult"
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Best Local Similarity 80.0%;
Matches. 28; Conservative
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Fax: +55-11-2707001
                                                 Conservative
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           Query Match
Best Local Similarity
Matches 29; Conserv
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AG112675.1 GI:16733194
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BARC Library clone:PTB-119B06.F.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehliro-Chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 bp mRNA linear EST 12-JAN-2001
BF813335 GI:12144616
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                   GSS 03-NOV-2001
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AG112675 687 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-119806.F, genomic survey sequence.
AG112675
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
                                                                                                                                                                                                                                                                                                      Fujiyama.A., Hattori,M., Toyoda.A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB Unpublished
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/clone_lib="PTB Chimpanzee Male BAC Library"
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/db_xref="taxon:9598"
/clone="PTB-119806.F"
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This and the control of the contro
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 390)
Aguero,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.
Aguero,F., verdun,B., Frasch,A.C.C. and Sanchez,D.O.
A random sequencing approach for the analysis of the trypanosoma
cruzi genome: general structure, large gene and repetitive DNA
families, and gene discovery
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Sep 14, 2000 this sequence version replaced gi:9371531.
Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
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CP(1650) San Martin, Prov. de BS AS. Argentina
Tel: 54-11-4580-7255 ext 309
                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
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GSSTGLIEGB Trypanosoma cruzi random genomic library Trypanosoma
cruzi genomic clone G41K6, DNA sequence.
AZ050757
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                                                                                                                       sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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8;
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Pred. No. 2.1e+02;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CI0148"
/dev_stage="Adult"
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Best Local Similarity 77.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               rel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trypanosoma cruzi.
                                                                              Simpson, A.J.
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TITLE
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A2856792 520 bp DNA linear GSS 21-FEB-200
2M0161P17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0161P17 F, DNA sequence.
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Unun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Fax: 54-11-4752-9639
Email: dsanchez@lib.unsam.edu.ar
Email: dsanchez@lib.unsam.edu.ar
Sequences were basecalled with phred and vector was masked with
crossmatch (see http://genome.washington.edu). Sequences were th
trimmed from both ends to remove low quality bases and masked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="CL-Brener"
/db_xref="taxon:5693"
/db_cxref="taxon:5693"
/clone="G41K6"
/clone="Ltype="epimastigote"
/clone=ltype="epimastigote"
/coll_type="epimastigote"
/coll_type=
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Pred. No. 2.2e+02;
0; Mismatches 8;
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Seg primer: CGTTGTAAAACGACGGCCAGT
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Location/Qualifiers
1. .520
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Insert Length: 10000 Std Erro
Plate: 0161 row: P column: 17
                                                                                                                                                                                                                                                                                                           class: shotgun.
   Location/Qualifiers
   1. 390
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77.1%;
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
1 (bases 1 to 520)
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Best Local Similarity 77.1%
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Fax: 801 585 7177
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mRNA sequence.
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ORIGIN
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JOURNAL
COMMENT
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KEYWORDS
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/Jab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114 jpblAF129072.1), a copy-number
inductible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for amplicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases I to 559)
Smith, T.P. L., Grosse, M.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Fertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.0%; Score 22; DB 12; Length 520; 73.7%; Pred. No. 2.8e+02; Live 0; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov
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/organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: 137 row: M column: 5
Seg primer: ATTTAGGTGACACTATAG.
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Best Local Similarity 73.74
Matches 28; Conservative
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Average insert 2: S kb. Library constructed by Life
Technologies, catalog # 12018 ol6. Investigators providing
samples: Lothar Hennighausen/Priscilla Furth, NIH
Reference for transgenic model: Li et al., Cell Growth and
Differentiation 7, 3-11 (1996). Note: this is a NCI_CGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BI659337 636 bp mRNA linear EST 12-SEP-2001 603301236F1 NIH_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5341856 5',
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NIH-WGC http://mgc.noi.nih.gov/.
                                                                                                       /note="Vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 20 and day 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM1868 row: g column: 09
High quality sequence start: 3
High quality sequence stop: 636.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
Emall: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
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Best Local Similarity 78.8
Matches 26; Conservative
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A1920579 350 bp mRNA linear EST 29-JUL-1999 618015G10.x1 618 - Inbred Tassel CDNA Library Zea mays CDNA, mRNA
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Inbred tassel library from Schmidt lab"
01 a 82 c 80 g 87 t
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropcgoneae; Zea.
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/lab_host="E.coli XL1-Blue MFR'"
/note="Organ: shoct; Vector: Lambda zap; Hake lab cDNA
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Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
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                   Contact: Walbot V
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 486048 row: B column: 02.
Location/Qualifiers
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Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 54.0%; Score 21.6; DB 9; Best Local Similarity 75.0%; Pred. No. 3.6e+02; Matches 27; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 ACTTGACCAAATCCTGACTGGGCTGGACCGGAGCG 292
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486048B02.x3 486 - leaf primordia cDNA library from Hake lab Zea
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486103A03.x1 486 - leaf primordia cDNA library from Hake lab Zea
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
1 (bases 1 to 230)
Walbot,V.
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1 (bases 1 to 343)
Malbot,V.
Malbot,V.
Malze ESTs from various cDNA libraries sequenced at Stanford University
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855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbotestanford.edu
Plate: 486103 row: A column: 03.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 21.6; DB 9;
Pred. No. 3.2e+02;
0; Mismatches 9;
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/lab_host="E.coli XL1-Blue MFR'"
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/organism="Zea mays"
/cultivar="B73"
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Matches 27; Conservative (
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Best Local Similarity 75.0°
Matches 27; Conservative
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486009G01.x2 486 - leaf primordia cDNA library from Hake lab Zea
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
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mmys cDNA, mRNA sequence.
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Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
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Unpublished (1999)
Contact: Walbot V
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 725 8227
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          DB 9;
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         54.0%; Score 21.6; DB 9; 75.0%; Pred. No. 3.6e+02; Live 0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 54.0%; Score 21.6; DB 9;
Best Local Similarity 75.0%; Pred. No. 3.8e+02
Matches 27; Conservative 0; Mismatches 9
                                                                                223 ACTTGACCAGATCCTGACTGGGCTGGACCGGGGGGCG 258
                                                                   5 acttgaccctactctacctgggctggactgggtggg 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            column: 01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: walbot@stanford.edu
Plate: 486009 row: G column
Location/Qualifiers
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                                                                                                                                                                                                   mays cDNA, mRNA sequence.
A1438418
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ag91c05.xl maize inflorescence immature ear library Zea mays cDNA clone ag91c06 3', mRNA sequence.
A1065660.1 GI:3341067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4577"
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; 2ea. | (basies 1 to 422) | Walbot; V. | Walbot; V. | Maize ESTs from various cDNA librarles sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="leaf primordia" ...
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/lab_host="E.col1 xl1-Blue MFK'"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 426)
Schutz.K., de la Bastide,M., Gnoj.L., Habermann,K., Huang,E.N.,
Parnell,L.D., Dedhia,N., Martienssen,R. and McCombie,W.R.
Expressed sequence tags from 2. mays
Unpublished (1998)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
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Pred. No. 3.8e+02;
); Mismatches 9; Indels
                                                                                                                          University
Unpublished (1999)
Contact: Walbot because the proof of Biological Sciences
Stanford University
B55 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 486068 row: G column: 02.
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75.0%; Pred. No. ...
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Seq primer: M13 forward universal -21
High quality sequence stop: 426.
Location/Qualifiers
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//Jissue_right="immature ear"
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//Iste_2: EcorR; This library is described in Schmidt, Hake,
et al., (1993) Plant Cell 5:729-737. CDNAs are
directionally cloned into the XhoI and EcoRI sites; XhoI
is near the polyA tail. Most reads from this library are
3' in direction. Additional information on this library as
well as ftp access to all sequences can be found at
http://www.cshi.org/maizegenome"
a 89 c 116 t 4 others
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AW917931
AW917931.1 GI:8083695
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liver, embryo, heart, muscle, spleen"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 437)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
/clone="ag91c06"
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/sex="female"
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Contact: Lee, NH
The Institute for Genomic Research
The Institute for Genomic Research
The 1019-883-3529
Fax: (301)-888-0208
Email: nhlee@tigr.org
Email: nhlee@tigr.org
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC tel#703-365-2700 for further information
Seq primer: M13 Reverse.
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Search completed: June 4, 2002, 17:09:02 Job time: 4535 sec

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Sequence Sequence Sequence Sequence Sequence

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US-08-061-465-1 US-09-434-774-11 US-09-009-913-1

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Sequence

Sequence 4 Sequence 4 Sequence 4

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APPLICANT: Hayden. Michael R.
APPLICANT: Hayden. Abigail
APPLICANT: How, A.H.M. Mahbubul
APPLICANT: Chopra, Vikramjit Singh
APPLICANT: Kalchman, Michael
TITLE OF INVENTION: Apoptosis Modulators That Interact with the
TITLE OF INVENTION: Huntington's Disease Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSE: Oppedahl & Larson
STREET: PO BOX 5270
CITY: Frisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA.
ZIP: 80443-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Larson, Marina T.
REGISTRATION NUMBER: 32038
REFERENCE/DOCKET NUMBER: UBC.P-013US2
TELECOMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,199B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon 15 of HIP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MS DOS 5.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Larson, Marina T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: genomic HYPOTHETICAL: no
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STRANDEDNESS: double
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ORGANISM: human
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CLASSIFICATION:
ANTI-SENSE: no
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 Sequence 1, Appli
Sequence 1, Appli
Sequence 179, App
Sequence 179, App
Sequence 13, Appl
Sequence 13, Appl
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Sequence 1, Appli
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                                                                       June 4, 2002, 17:47:11 ; Search time 116.71 Seconds (without alignments) 84.186 Million cell updates/sec
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US-08-21B-208-23
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US-08-24B-273A-47
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Maximum Match 100%
Listing first 45 summaries
                                                    nucleic search, using sw model
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          GenCore
Copyright (c) 1993
                                                                                                              US-09-721-543A-14
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length: 2000000000
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APPLICANT: Hayden. Michael R.
APPLICANT: Hackam, Abigail
APPLICANT: Hackam, Abigail
APPLICANT: Hoptora, Vikamijit Singh
APPLICANT: Chopra, Vikamijit Singh
APPLICANT: Kalchman, Michael
APPLICANT: Kalchman, Michael
TITLE OF INVENTION: Apoptosis Modulators That Interact with the TITLE OF INVENTION: Huntington's Disease Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: CDNA for Huntington-interacting protein US-09-085-1998-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 4796;
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                                                                                                                                                                                                                                                                                               STATE: CO
COUNTRY: USA
COUNTRY: USA
COMPUTER READAULE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1. Application US/08996306
Sequence 1. Application US/08996306
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
TITLE OF INVINTION: Prostate cancer gene
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20.2; DB Pred. No. 23; 0; Mismatches
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501 West Broadway
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                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: MS DOS 5.0
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,199B
Sequence 3, Application US/09085199B
                                                                                                                                                                                                                                        ADDRESSEE: Oppedahl & Larson
STREET: PO BOX 5270
CITY: Frisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Larson, Marina T.
REGISTRATION NUMBER: 32038
REFERENCE/DOCKET NUMBER: UB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (970) 668-2050
TELEFAX: (970) 668-2052
INFORMATION FOR SEG ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.5%;
ilarity 75.8%;
Conservative
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STRANDEDNESS: singl
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                  Patent No. 6235879
GENERAL INFORMATION:
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Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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US-08-996-306-1
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APPLICANT: Hayden. Michael R.
APPLICANT: Hackan, Abigail
APPLICANT: Hackan, Abigail
APPLICANT: Hope, A.H.M. Mabhabull
APPLICANT: Chopra, Vikramjit Singh
APPLICANT: Kalchman, Michael
TITLE OF INVENTION: Apoptosis Modulators That Interact with the
NUMBER OF SEQUENCES: 44
CORRESPONDENCE: ADDRESS:
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                                     Length 359;
                                                                            Indels
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MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
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                                     DB 4;
                                 Score 20.2; DE Pred. No. 14; 0; Mismatches
                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS DOS 5.0
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,199B
                                                                                                                                                                                                                                                       Sequence 1, Application US/09085199B Patent No. 6235879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: PO BOX 5270
CITY: Frisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: LAISON, MAINE TON RESTRATION NUMBER: 32038
REFIRENCE/DOCKET NUMBER: UBC.)
TELEPCOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                 Query Match 50.5%;
Best Local Similarity 75.8%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA HYPOTHETICAL: no
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Matches 25; Conserv
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US-09-085-199B-1/C
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US-09-085-199B-3/c
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SOFTWARE: WOLD

CURRENT APPLICATION DATA:

PAPLICATION NUMBER: US/08/996,306
FILING DATE:
CLASSIFICATION:
ATTORNEY/FAGENT INFORMATION:
NAME: ISTABLSEN, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/COCKET NUMBER: 29,655
REFERENCE/COCKET NUMBER: GENSET.018A
REFERENCE/COCKET NUMBER: GENSET.018A
TELECOMMUNICATION INFORMATION:
TELEPRONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
LENGTH: 56516 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
MOLECULE TYPE: GENOMIC DNA
ORGANISM: HOMO SADIENS
FRAURE:
FRAURE:
RAUGH AND SADIENS
FRAURE:
FRA
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LOCATION: 1679..1870
IDENTIFICATION METHOD: Proscan
PEATURE:
NAME/KEY: Potential ATG
LOCATION: 1998..2000
                                                      COUNTRY: USA
ZIE: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
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compl(13962..13981)
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11930..11947
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11694..14332
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12057..12103
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18196..18265
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23717..23832
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2031..2033
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2001..2216
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San Diego
California
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FEATURE:
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NAME/KEY:
LOCATION:
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48.5%; Score 19.4; DB 2;
Best Local Similarity 79.3%; Pred, No. 71;
Matches 23; Conservative 0: Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Cohen, Dantel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
TITLE OF INVENTION: PROSTATE CANCER GENE
TITLE REFERENCE: GENSET.18CPICP
CURRENT APPLICATION NUMBER: US/09/318, 907
CURRENT FILING DATE: 1999-06-23
EARLIER APPLICATION NUMBER: 08/996,3(6
EARLIER FILING DATE: 1997-12-22
BARLIER FILING DATE: 1998-09-09
EARLIER FILING DATE: 1998-09-09
EARLIER FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 578
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US-09-338-907-1
; Sequence 1, Application US/09338907
; Patent No. 6265546
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                                                                                                  compl(34625..34645)
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compl(51482..51499)
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54445..54450
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51149..51168
SEQ ID43
34216..34234
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34669..34759
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40688..40846
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48070..48193
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50182..54523
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51596..51613
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51612..51658
                                          SEQ ID25
34469..34515
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51448..51494
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NAME/KEY:

LOCATION:

US-08-996-306-1
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OTHER INFORMATION: upstream amplification primer 4-65 SEQ ID65
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NAME/KEY: primer_bind
LOCATION: 51996..52015
OTHER INFORMATION: downstream amplification primer 4-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: primer_bind
LOCATION: 51482..51499
OTHER INFORMATION: downstream amplification primer 4.65
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NAME/KEY: primer_bind
LOCATION: 51596..51613
OTHER INFORMATION: upstream amplification primer
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OTHER INFORMATION: polymorphic fragment 4-67
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Pred. No. 71;
0; Mismatches
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Patent No. 6346331
GENERAL INFORMATION:
APPLICANT: COhen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Prostate cancer gene
FILE REFERENCE: GENEST: 018021
CURRENT APPLICATION NUMBER: US/09/218, 207
CURRENT FILING DATE: 1998-12-22
EARLIER APPLICATION NUMBER: 60/099, 658
EARLIER APPLICATION NUMBER: 60/099, 658
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Best Local Similarity 79.3%;
Matches 23; Conservative
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; LCCATION: 54445., 54450
; OTHER INFORMATION: AATAAA
US-09-338-907-1
                                                                  OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                       INFORMATION: exon
                                                                                                                                               OTHER INFORMATION: exon
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                            NAME/KEY: exon
LOCATION: 34669..34759
                                                                                                       NAME/KEY: exon
LOCATION: 40688..40846
                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 48070..48193
                                                                                                                                                                                                                                                                                     LOCATION: 50182..54523
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LOCATION: 51448..51494
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LOCATION: 51612..
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LOCATION: 34625..34645
OTHER INFORMATION: downstream amplification primer 99-217 SEQ ID52, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement
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LOCATION: 13962..13981
OTHER INFORMATION: downstream amplification primer 4-73 SEQ ID67,
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LOCATION: 13547..13564
OTHER INFORMATION: upstream amplification primer 4-73 SEQ
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LOCATION: 34469..34515
OTHER INFORMATION: polymorphic fragment 99-217 SEQ ID25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4-77
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OTHER INFORMATION: downstream amplification primer
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LOCATION: 11930..11947
OTHER INFORMATION: upstream amplification primer
                                                                                                                   NAME/KEY: promoter
LOCATION: 1629..1870
OTHER INFORMATION: identification method Proscan
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LOCATION: 13657..13703
OTHER INFORMATION: polymorphic fragment 4-73
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LOCATION: 34216..34234
OTHER INFORMATION: upstream amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: 12057..12103
OTHER INFORMATION: polymorphic fragment
                                                                                                                                                                                                                      LOCATION: 1998..2000
OTHER INFORMATION: potential start codon
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LOCATION: 11694..14332
OTHER INFORMATION: Tyr Phos
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LOCATION: 2001..2216
OTHER INFORMATION: exon1
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OTHER INFORMATION: exon
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LOCATION: 2031..2033
OTHER INFORMATION: ATG
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LOCATION: 1998..2000
                                                                             ORGANISM: Homo sapiens
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LOCATION: 18196..18265
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LOCATION: 12339..1235
SOFTWARE: Patent.pm
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                      SEQ ID NO 1
LENGTH: 56516
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OTHER INFORMATION: downstream amplification primer 99-217 SEQ ID52, FEATURE:
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NAME/KEY: primer_bind
LOCATION: 51149..51168
OTHER INFORMATION: upstream amplification primer 4-65
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OTHER INFORMATION: polymorphic fragment 4-67
FEATURE:
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NAME/KEX: primer_bind
LCCATION: 51596..51613
OTHER INFORMATION: upstream amplification
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Sequence 179, Application US/09338907
Sequence 179, Application US/09338907
Sequence 179, Application US/09338907
Sequence 179, Application US/09338907
Setcht No. 6265346
Septicant: Ochen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Budgueleret, Lydie
TITLE OF INVENTION: PROSTATE CANCER GENE
FILE REFERENCE: GENSET. 18CPLCP
CURRENT APPLICATION NUMBER: US/09/338,907
CURRENT FILING DATE: 1999-06-23
EARLIER APPLICATION NUMBER: 08/996,306
SEARLIER APPLICATION NUMBER: 60/099,658
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele
COCATION: 51448..51494
OTHER INFORMATION: polymorphic fragment
FEATURE:
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LOCATION: 51482..51499
OTHER INFORMATION: downstream
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LOCATION: 51996..52015
OTHER INFORMATION: downstream
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Best Local Similarity 79.35
Matches 23; Conservative
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NAME/KEY: polyA_signal
LOCATION: 54445.54450
OTHER INFORMATION: AATAAA
                                                             LOCATION: 34669.34759
OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
                                                                                                                 NAME/KEY: exon
LOCATION: 40688..40846
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LOCATION: 13962..13981
OTHER INFORMATION: downstream amplification primer 4-73 SEQ ID67, complement
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LOCATION: 13547..13564
OTHER INFORMATION: upstream amplification primer
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LOCATION: 34469..34515
OTHER INFORMATION: polymorphic fragment 99-217
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LOCATION: 12057. 12103
OTHER INFORMATION: POlymorphic fragment 4-77
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LOCATION: 13657..13703
OTHER INFORMATION: Polymorphic fragment 4-73
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OTHER INFORMATION: downstream amplification
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OTHER INFORMATION: upstream amplification
                                                                                                                                NAME/KEY: promoter
LOCATION: 1629..1870
OTHER INFORMATION: identification method
                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 1998..2000
OTHER INFORMATION: potential start codon
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OTHER INFORMATION: upstream
   NUMBER OF SEQ ID NOS: 578
SOFTWARE: Patent.pm
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LOCATION: 23717..23832
OTHER INFORMATION: exon
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LOCATION: 25571..25660
OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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LOCATION: 11694..14332
OTHER INFORMATION: Tyr
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LOCATION: 18196..18265
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LOCATION: 34625..34645
                                                                                              ORGANISM: Homo sapiens
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                                        SEQ ID NO 1
LENGTH: 56516
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OTHER INFO
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NAME/KEY: primar_bind
LOCATION: 8560..8578
OTHER INFORMATION: upstream amplification primer 99-619 , complement
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LOCATION: 12013..12037
OTHER INFORMATION: downstream amplification primer 4-76 , complement
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LOCATION: 12339..12358
OTHER INFORMATION: downstream amplification primer 4-77 , complement
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OTHER INFORMATION: downstream amplification primer 4-71 , complement
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LOCATION: 13617..13636
OTHER INFORMATION: downstream amplification primer 4-72 , complement
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LOCATION: 13962..13981
OTHER INFORMATION: downstream amplification primer 4-73 , complement
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LOCATION: 18423..18442
OTHER INFORMATION: downstream amplification primer 4-90 , complement
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OTHER INFORMATION: upstream amplification primer 99-610 , complement
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LOCATION: 17814..17832
OTHER INFORMATION: upstream amplification primer 99-609 , complement
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LOCATION: 15994..16011
OTHER INFORMATION: downstream amplification primer 99-610
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LOCATION: 17304..17324
OTHER INFORMATION: downstream amplification primer 99-609
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LOCATION: 18699..18716
CHER INFORMAGION: downstream amplification primer 99-607
FEATURE:
                                                                                                                  FEATURE:
NAME/KEY: primer_bind
LOCATION: 11622..11639
OTHER INFORMATION: upstream amplification primer 4-76
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LOCATION: 11933..11947
OTHER INFORMATION: upstream amplification primer 4-77
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LOCATION: 12915..12932
OTHER INFORMATION: upstream amplification primer 4-71
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LOCATION: 13216..13233
OTHER INFORMATION: upstream amplification primer 4-72
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LOCATION: 13547..13564
OTHER INFORMATION: upstream amplification primer 4-73
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LOCATION: 18008..18027
OTHER INFORMATION: upstream amplification primer 4-90
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LOCATION: 13317..13334
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LOCATION: 4528..4546
OTHER INFORMATION: upstream amplification primer 99-622 , complement
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LOCATION: 2505..2525
OTHER INFORMATION: downstream amplification primer 5-63 , complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: primer_bind
LOCATION: 5927..5947
OTHER INFORMATION: upstream amplification primer 99-621 , complement
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LOCATION: 8127..8144
OTHER INFORMATION: downstream amplification primer 99-619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: primer_bind
LOCATION: 4091..4111
OTHER INFORMATION: downstream amplification primer 99-622
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LOCATION: 5475..5495
OTHER INFORMATION: downstream amplification primer 99-621
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LOCATION: 1991..2008
OTHER INFORMATION: upstream amplification primer 5-63
EARLIER FILING DATE: 1998-09-09
EARLIER APPLICATION NUMBER: 09/218,207
EARLIER FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 578
SOCTWARE: PATENT. pm
SEQ ID NO 179
LENGTH: 56520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: polyA_signal
LOCATION: 54493..54498
OTHER INFORMATION: AATAAA
                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 18196..18265
OTHER INFORMATION: exon2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: exon
LOCATION: 34668.34758
OTHER INFORMATION: exon5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 50179..54519
OTHER INFORMATION: exon8
                                                                                                                                                                                                                                                                               NAME/KEY: exon
LOCATION: 2001..2216
OTHER INFORMATION: exon1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: exon
LOCATION: 25570..25659
OTHER INFORMATION: exon4
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LOCATION: 48067..48190
OTHER INFORMATION: exon7
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LOCATION: 40685..40843
                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: exon
LOCATION: 23716..23831
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NAME/KEY: exon
LOCATION: 18196..18265
OTHER INFORMATION: exon2
                                                   LOCATION: 2001..2216
OTHER INFORMATION: exon1
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LOCATION: 25657..25674
OTHER INFORMATION: upstream amplification primer 99-600 , complement
                                                                                                                                                                      FEATURE:
NAME/KEY: primer_bind
LOCATION: 23111._23129
OTHER INFORMATION: upstream amplification primer 99-602 , complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: primer_bind
LOCATION: 27022..27040
OTHER INFORMATION: upstream amplification primer 99-598 , complement
                                                 OTHER INFORMATION: upstream amplification primer 99-607 , complement
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79.3%; Pred. No. 71;
tive 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                NAME/KEY: primer_bind
LOCATION: 25098..25118
OTHER INFORMATION: downstream amplification primer 99-600
                                                                                             NAME/KEY: primer_bind
LOCATION: 22589..22609
OTHER INFORMATION: downstream amplification primer 99-602
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OTHER INFORMATION: downstream amplification primer 99-598
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LOCATION: 32262..32281
OTHER INFORMATION: downstream amplification primer 99-592
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LOCATION: 34215..34233
OTHER INFORMATION: upstream amplification primer 99-217
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| Patent No. 6346381
| GENERAL INFORMATION:
| APPLICANT: Cohen, Daniel APPLICANT: Cohen, Daniel APPLICANT: Bougueleret, Lydie TITLE OF INVENTION: Prostate cancer gene FILE REFERENCE: GRNSET. 018CP1
| CURRENT APPLICATION NUMBER: US/09/218, 207 CURRENT FILING DATE: 1998-12-22
| EARLIER FILING DATE: 1998-10-109
| NUMBER OF SEQ ID NOS: 578
| SEQ ID NO 179
| LENGTH: 56520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2735 ccaactttaactgggcttgaatgtgtggg 2763
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Matches 23; Conservative
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ORGANISM: Homo sapiens
NAME/KEY: primer_bind
LOCATION: 19164..19182
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LOCATION: 32823..32841
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US-09-218-207-179
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NAME/KEY: primer_bind
LOCATION: 4528..4546
OTHER INFORMATION: upstream amplification primer 99-622 , complement
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LOCATION: 2505..2525
OTHER INFORMATION: downstream amplification primer 5-63 , complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: upstream amplification primer 99-621 , complement
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LOCATION: 4091..4111
OTHER INFORMATION: downstream amplification primer 99-622
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LOCATION: 8127..8144
OTHER INFORMATION: downstream amplification primer 99-619
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LOCATION: 5475..5495
OTHER INFORMATION: downstream amplification primer 99-621
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LOCATION: 1991..2008
OTHER INFORMATION: upstream amplification primer 5-63
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LOCHENTION: 11622..11639
OCHER INFORMATION: upstream amplification primer 4-76
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: polya_signal
LOCATION: 54493..54498
OTHER INFORMATION: AATAAA
                                                                                                                                                                                                                          NAME/KEY: exon
LOCATION: 34668..34758
OTHER INFORMATION: exon5
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VIDE.
FEATURE:
NAME/KEY: exon
TOTAL 23116..23831
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FOCATION: 50179..54519
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                                                                                                                                NAME/KEY: exon
LOCATION: 25570..25659
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LOCATION: 5927..5947
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LOCATION: 8560..8578
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LOCATION: 23111..23129
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US-08-123-161A-13
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                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Upstream amplification primer 4-71
FERTURE:
NAME/KEY: primer_bind
LOCATION: 13317..13334
OTHER INFORMATION: downstream amplification primer 4-71 , complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: primer_bind
LOCATION: 13617..13636
OTHER INFORMATION: downstream amplification primer 4-72 , complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: primer_bind
LOCATION: 13962.13981
OTHER INFORMATION: downstream amplification primer 4-73 , complement
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LOCATION: 18423.18442
OTHER INFORMATION: downstream amplification primer 4-90 , complement
                                                                                                                                                                                                                       LOCATION: 12339.712358
OTHER INFORMATION: downstream amplification primer 4-77 , complement
FERTURE: primer_bind
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LOCATION: 19164..19182
OTHER INFORMATION: upstream amplification primer 99-607 , complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 16463.16480
OTHER INFORMATION: upstream amplification primer 99-610 , complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 17814._17832
OTHER INFORMATION: upstream amplification primer 99-609 , complement
                                                   OTHER INFORMATION: downstream amplification primer 4-76 , complement
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OTHER INFORMATION: downstream amplification primer 99-602
FEATURE:
NAME/KEY: primer_bind
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OTHER INFORMATION: downstream amplification primer 99-610
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OTHER INFORMATION: downstream amplification primer 99-609
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LOCATION: 18699..18716
OTHER INFORMATION: downstream amplification primer 99-607
                                                                   FEATURE:
NAME/KEY: primer_bind
NAME/KEY: 11930..11947
OTHER INFORMATION: upstream amplification primer 4-77
FEATURE:
NAME/KEY: primer_bind
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LOCATION: 18008..18027
OTHER INFORMATION: upstream amplification primer 4-90
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OTHER INFORMATION: upstream amplification primer 4-72
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NAME/KEY: primer_bind
LOCATION: 12018..12037
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LOCATION: 13547..13564
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Sequence 13, Application US/08123161A

Patent No. 5449616

GENERAL INFORMATION:
APPLICANT: Campbell, Kevin P.
APPLICANT: Anderson, Richard D.
APPLICANT: Anderson, Richard D.
APPLICANT: Anderson, Richard D.
APPLICANT: Yang, Bin
TITLE OF INVENTION: NUCLEIC ACID ENCODING DYSTROPHIN-ASSOCIATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
OTHER INFORMATION: upstream amplification primer 99-602 , complement
                                                                                                                                                          NAME/KEY: primer_bind
LOCATION: 25657..25674
OTHER INFORMATION: upstream amplification primer 99-600 , complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: primer_bind
LOCATION: 32823...32841
OTHER INFORMATION: upstream amplification primer 99-592 , complement
                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 27022...27040
OTHER INFORMATION: upstream amplification primer 99-598 , complement
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79.3%; Pred. No. 71;
tive 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: primer_bind
LOCATION: 32262..32281
OTHER INFORMATION: downstream amplification primer 99-592
                                               NAME/KEY: primer_bind
LOCATION: 2509E. 25118
OTHER INFORMATION: downstream amplification primer 99-600
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NAME/KEY: primer_bind
LOCATION: 26537..26557
OTHER INFORMATION: downstream amplification primer 99-598
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NAME/KEY: primer_bind
LOCATION: 34215..34233
OTHER INFORMATION: upstream amplification primer 99-217
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,161A
FILING DATE: 16-SEP-93
CLASSIFOATION: 435
PRIOR APPLICATION DATA:
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LOCATION: 34624..34644
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LOCATION: 27022...2704
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Gaps
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Fatent No. 5255049
GENERAL INFORMATION:
APPLICANT: Monroe, Stephan S.
APPLICANT: Roopmans, Marion
APPLICANT: Roopmans, Marion
APPLICANT: Stephan S.
TITLE OF INVENTION: BENOTINE IN SEROTYPE II AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: 127 Peachtree Street, N.E.
STREET: Suite 1200
CITY: Atlanta
STATE: Geordia
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                                                                                                                                                                         Length 2389;
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Sequence 11, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Ornust, Rene
APPLICANT: Ornust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: and Methods For Pheir Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.5%; Score 19; DB 3; Length 969; 71.4%; Pred. No. 51; tive 0; Mismatches 10; Indels
                                                                                                                                                                                                               Indels
                                                                                                                                                                   Score 19.2; DB 1;
Pred. No. 50;
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                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                               3 tcacttgaccctactctacctgggctggactg 34
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COMPUTER: IBM PC compatible
                                                                                                                                                                       Query Match 48.0%;
Best Local Similarity 75.0%;
Matches 24; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 71.4
Matches 25; Conservative
             double
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                                                                               ), NAME/KEY: CDS
; LOCATION: 106..1620
US-08-483-278-13
                          TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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ZIP: 30303-1811
             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: mouse
US-09-188-930-11
                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-09-188-930-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 11
LENGTH: 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-061-465-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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APPLICANT: Campbell, Kevin P.
APPLICANT: Enaghimov, Oxana B.
APPLICANT: Evasti, James M.
APPLICANT: Levelile, Cynthia J.
TITLE OF INVENTION: NUCLEIC ACID ENCODING DYSTROPHIN-ASSOCIATED VITLE OF INVENTION: PROTEIN NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                       Length 2389;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
APPLICATION NUMBER: 07/946,234
FILING DATE: 14-SEP-92
ATTORNEY/AGENT INFORMATION:
NAME: FAITELL, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: UIRF89-11A4
TELEPAN: (207) 363-0558
TELEPAN: (207) 363-0528
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2389 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1786 TCACTGGACCCTGCCCGTGCTGGGGTGGCCTG 1817
                                                                                                                                                                                                                                                                                                                                                                                                      Score 19.2;
Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 tcacttgaccctactctacctgggctggactg 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/08483278 Patent No. 5686073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,161
FILLING DATE: 16-SEP-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 48.0%;
Best Local Similarity 75.0%;
Matches 24; Conservative (
                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
, LOCATION: 106..1620
US-08-123-161A-13
                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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Sequence 53, Application US/08486273A
Sequence 53, Application US/08486273A
Sequence 53, Application US/08486273A
Sequence 53, Application US/08486273A
Sequence 53, Application Sequence 53
GENERAL INFORMATION:
APPLICANT: Blis, Steven B.
APPLICANT: Lu, Chin-Chun W.
APPLICANT: Lu, Chin-Chun W.
TITLE OF INVEHTION: HUMAN N-METHYL-D-ASPARTATE RECEPTRO SUBUNITS, DNA TITLE OF INVEHTION: BACODING SAME AND USES THEREFOR NUMBER OF SEQUENCES: 63
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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COUNTRY: U.S.A.
21P: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: SM PC COMPATIBLE
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATION DATA:
APPLICATION NUMBER: US/08/486,273A
FILING DATE: 06-70N-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/231,193
FILING DATE: O-APR-1994
CLASSIFICATION: Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
RELEPRAKE 619-238-0999
TELEFRAK: 619-238-0062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 47.5%; Score 19; DB 2; Le Best Local Similarity 71.4%; Pred. No. 65; Matches 25; Conservative 0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
                                                                              INFORMATION FOR SEQ ID NO: 53
SEQUENCE CHARACTERISTICS:
LENGTH: 4002 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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; LOCATION: 189..3833
US-08-231-193A-53
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                         TOPOLOGY: both
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                      both
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STATE:
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: Sequence 53, Application US/08231193A
: Sequence 53, Application US/08231193A
: Patent No. 5849895
: Patent No. 5849895
: GENERAL INFORMATION:
APPLICANT: Elia, Steven B.
APPLICANT: Lia, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: GROWN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION:
TITLE OF INVENTION
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/061,465
FILING DATE: 19930512
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: PEFTYMENT DAVID G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.069
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2515 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGIE
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,193A
FILING DATE: 20-APR-1994
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Seldman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,459
FILING DATE: 20-APR-1993
CLASSIFICATION: 536
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STRAIN: Serotype 2
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MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
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US-08-061-465-3
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Edgett, Lorrie P.
APPLICANT: Edgett, Lorrie P.
APPLICANT: Liaw, Chen W.
APPLICANT: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA ENCODING
TITLE OF INVENTION: AMETHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA ENCODING
TITLE OF INVENTION: AMETHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA ENCODING
TITLE OF INVENTION: AMETHYL, Haller & McClain
STREET: L660 Union Street
CITY: San Diego
STRAFE: A CONMUTER: L1aw PC compatible
COMPUTER: L1aw PC compatible
COMPUTER: PAPELICATION DATA:
COMPUTER: PAPELICATION DATA:
APPLICATION NUMBER: US/08/480,474
FILING DATE: 06-JUN-1995
CLASSIFICATION: SANG
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                                                                                          Query Match 47.5%; Score 19; DB 2; Length 4002; Best Local Similarity 71.4%; Pred. No. 65; Matches 25; Conservative 0; Mismatches 10; Indels
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NAME: Seidman, Stephante
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9382B
TELECOMMUNICATION INFORMATION:
TELEFAX: 619-238-0999
TELEFAX: 619-238-0909
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 4002 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: June 4, 2002, 17:47:23
Job time: 6596 sec
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LOCATION: 189..3833
US-08-480-474-53
189..3833
; LOCATION:
US-08-486-273A-53
                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-480-474-53
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#11347 for g brain expres brain expres bone marrow

Human Human Human

Human bone marrow Probe #1677 for ge Probe #10670 for ge Probe #1460 used t Probe #1431 used t Probe #6428 used t Cat flea head and Human APOBEC2 gene Human APOBEC2 gene

Human colon cancer
Human breast cance
Human breast and o
Erythrobacter long
Human Immune/haema
Human Immune/haema

Human musculoskele

Murine interferon

Human immune/haema Human immune/haema

Human digestive sy Drosophila melanog Human PG-3 gene.

Polynucleotide ligands useful as anti-viral agents for the treatment of

WPI; 2001-367658/38

liver foetal liver for ge

Human foetal Probe #1442 1

Human Human

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Fusarium venenatum Helicobacter pylor H. pylori GHPO 144 Drosophila melanog Human immune/haema

Human immune/haema

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Sequence:

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Scoring table:

Searched:

Minimum DB : Maximum DB :

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Ligand; human cytomegalovirus; HCMV infection; herpetic ulcer; pneumonia; gastroenteritis; chorloretinitis; antiviral agent;
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                                                      AAK26895
AAK39928
AAI11524
AAI20737
AAI32801
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AA101440
AA106437
AAC93601
AAD25770
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AAK85255
AAI61050
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ABL23386
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AAK81332
AAH36788
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ABL22618
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AAS53753
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AAK59097
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Synthetic.
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  RESULT
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DNA ligand #8 for
Human musculoskele
Human musculoskele
                                                                                                                         4, 2002, 17:56:19 ; Search time 521.5 Seconds (without alignments) 131.690 Million cell updates/sec
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breast cell
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| SIDSI/gcgdata/geneseq/genesegn-embl/NA1980.DAT:*
| SIDSI/gcgdata/geneseq/genesegn-embl/NA1981.DAT:*
| SIDSI/gcgdata/geneseq/genesegn-embl/NA1981.DAT:*
| SIDSI/gcgdata/geneseq/genesegn-embl/NA1981.DAT:*
| SIDSI/gcgdata/geneseq/genesegn-embl/NA1981.DAT:*
| SIDSI/gcgdata/geneseq/genesegn-embl/NA1985.DAT:*
| SIDSI/gcgdata/geneseq/genesegn-embl/NA1986.DAT:*
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                1736436 seqs, 858457221 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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ABA47902
ABA53200
ABA65792
ABA62796
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AAL37595

    nucleic search, using sw model

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AAD10602
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40
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seq length: 200000000
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Match Length
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Claim 8; Page 6; 60pp; English.
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18-APR-2000;
19-MAY-2000;
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30-JUN-2000;
07-JUL-2000;
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11-JUL-2000; 2
11-JUL-2000; 5
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14-AUG-2000;
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14-AUG-2000;
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                                                                                                                                                                                                                                                                          Gaps
herpesvirus infections e.g. primary or chronic infections with human
                                                                  The invention relates to polynucleotide ligands which bind to herpesvirus, particularly human cytomegalovirus (HCMV) to decrease or block HCMV infection in target cells. These ligands are used as anti-viral agents for the treatment of herpesvirus infections (e.g. lesions and herpetic ulcers) and particularly HCMV associated primary or chronic infections such as pneumonia, gastroenteritis and chorioretinitis. The present sequence is DNA ligand which bind to HCMV to decrease or block HCMV infection in target cells.
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/note= "This residue is absent in the sequence
shown as SEQ ID NO:16 in the sequence listing
of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ligand; human cytomegalovirus; HCMV infection; herpetic ulcer; pneumonia; gastroenteritis; chorioretinitis; antiviral agent; herpesvirus infection; lesion; ds.
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                                                                                                                                                                                                                                             Length 40;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note- "This residue is absent in the
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                                                                                                                                                                                                                                                                                                   1 ctatttcccacccatatccccttgggcccttgggtgtggg 40
                                                                                                                                                                                                                                          100.0%; Score 40; DB 22;
100.0%; Pred. No. 1.3e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                 Sequence 40 BP; 4 A; 14 C; 10 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA ligand #8 for human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                        Claim 8; Page 6; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  AAD10602 standard; DNA; 40 BP
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Best Local Similarity 100.
Matches 40; Conservative
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              cytomegalovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
The invention relates to polynucleotide ligands which bind to herpesvirus, particularly human cytomegalovirus (HCMV) to decrease or block HCMV infection in target cells. These ligands are used as anti-viral agents for the treatment of herpesvirus infections (e.g. lesions and herpetic ulcers) and particularly HCMV associated primary or chronic infections such as pneumonia, gastrometeritis and chorioretinitis. The present sequence is DNA ligand which bind to HCMV to decrease or block HCMV infection in target cells.
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                                                                                                                                                                                                                                                                             Sequence 40 BF; 5 A; 15 C; 6 G; 11 T; 3 other;
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AAL37594/c
ID AAL37594 standard; DNA; 8439 BP.
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2000US-0217487.
2000US-0217496.
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2000US-0225266.
2000US-0225267.
2000US-0225268.
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2000US-0184664
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2000US-0209467
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2000US-0236368
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                                     22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
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01-SEP-2000,
01-SEP-2000,
05-SEP-2000,
06-SEP-2000,
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08-SEP-2000,
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18-AUG-2000;
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25-SEP-2000;
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14-SEP-2000;
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27-SEP-2000;
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29-SEP-2000;
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20000S-0246610 2000US-0246613 2000US-0249207. 2000US-0249208. 2000US-0249209. 2000US-0249210. 2000US-0249211 2000US-0249213 2000US-0249214 2000US-0249215 2000US-0249218 20000S-0249244 20000S-0249245 2000US-0249300 2000US-0250160. 2000US-0250391. 2000US-0251030 2000US-0256719 2000US-0251479 2000US-0251856 2000US-0251868 2000US-0251990 2000US-0249264 08-NOV-2000; 08-NO

(HUMA-) HUMAN GENOME SCI INC.

SM Rosen CA, Barash SC,

WPI; 2001-451937/48.

Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis

Example 2; SEQ ID NO 3959; 781pp + Sequence Listing; English.

The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliotating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (art)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune chisorders e.g. Addison's alsease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular discenses such as myocardial ischaemias; (d) wound parasitic infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.WIPO.int/Pub/Published_pct_sequences.

Sequence 8439 BP; 1748 A; 2333 C; 2307 G; 2051 T; 0 other;

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20000S-0231242.
20000S-0231243.
2000US-0231244.
2000US-0231244.
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2000US-0232397.
2000US-0232398.
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2000US-0232080.
2000US-0232081.
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2000US-0232401.
2000US-0233063.
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2000US-0233065.
2000US-0234223.
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2000US-0234997.
2000US-0234998.
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2000US-0241221.
2000US-0241785.
2000US-0241786.
2000US-0241786.
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2000US-0237037.
2000US-0237038.
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2000US-0239935.
2000US-0239937.
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2000US-0246476.
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2000US-0246477.
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2000US-0246524.
2000US-0246525.
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2000US-0230438
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2000US-0236370
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01-SEP-2000

05-SEP-2000

06-SEP-2000

06-SEP-2000

06-SEP-2000

06-SEP-2000

06-SEP-2000

08-SEP-2000

09-SEP-2000

09-SEP-2000

00-OCT-2000

00-OC
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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                                                                                                                                                                                                                                                                Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; musculoskeletal system; ds.
                                                    Gaps
                                                                                                                                                                                                                                        Human musculoskeletal system related polynucleotide SEQ ID NO 3960.
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                       Score 22; DB 22; Length 8439;
Pred. No. 33;
0; Mismatches 5; Indels
                                                                                       7 cccacccatatccccttgggcccttgggtg 36
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AAL37595/c
ID AAL37595 standard; DNA; 9875
                      55.0%;
83.3%;
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2000US-0190076
2000US-0205515
2000US-0205515
2000US-020467
2000US-0215135
2000US-021647
2000US-021647
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2000US-021647
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2000US-0220963.
2000US-0220964.
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20000S-0225214.
20000S-0225266.
20000S-0225267.
20000S-0225267.
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2000US-0225447.
2000US-0225757.
2000US-0225757.
          Ouery Match
Best Local Similarity 83.33,
Best Local 25; Conservative
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
11-MAR-2000;
11-MAR-2000;
19-MAY-2000;
07-JUN-2000;
30-JUN-2000;
30-JUN-2000;
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07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
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New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human
                                                                                                                       Human; microarray; single exon probe; gene expression; breast;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1470; 327pp + sequence listing; English.
                                                                                            Human breast cell single exon nucleic acid probe #1470.
ABA42775/C
ID ABA42775 standard; DNA; 455 BP.
                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                       disease; cancer; ss.
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                                                                                                                                                                                         WO200157271-A2.
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21-SEP-2000;
27-SEP-2000;
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30-JUN-2000;
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                                        ABA42775;
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                                          8XXCCCCCCCCCCCCCCCX8XBBZXBXBXBBBBBBXBXBXBXBXBXBBXBXXBXXBXAXB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               paralitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; SEQ ID NO 3960; 781pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                             Barash SC, Ruben SM
                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                     2000US-0251030
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                                                     2000US-0249217
                                                                                                           2000US-0249264
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17-NOV-2000;
17-NOV-2000;
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-DEC-2000;
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17-NOV-2000;
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                                                    17-NOV-2000;
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06-DEC-2000;
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Rank DR;

Chen W,

Hanzel DK,

2000US-0632366. 2000US-0234687. 2000US-0236359. 2000US-0207456 2000US-0608408

2000GB-0024263

2001WO-US00662

(first entry)

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and Br 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microariay. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for edetermining predisposition and/or prognosing breast disease. Gene expression analysis is useful for each sissessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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Matches 28; Conservative
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Query Match Best Local Si Matches 25;

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Score 22; DB 22; Length 9875; Pred. No. 34;

55.0%;

ABA47902;

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Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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llarity 71.8%; Pred. No. 37;
Conservative 0; Mismatches 11; Indels 0
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2000US-0234687.
2000US-0236359.
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2000US-0608408.
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                                                                                  (first entry)
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Matches 28; Conserv
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30-JUN-2000;
03-AUG-2000;
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27-SEP-2000;
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                                ABA53200;
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                                                                                                                                                                                                              microarray; single exon probe; gene expression; breast;
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                                                                                                                                                    Human breast cell single exon nucleic acid probe #6597
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0; Mismatches
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ABA47902 standard; DNA; 455 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-UJN-2000; 2000US-0693408.
03-AUG-2000; 2000US-0234687.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-023459.
04-OCT-2000; 2000GB-0024263.
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                                                                                                     (first entry)
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Matches 28; Conservative
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                                                                                                                                                                                                                                         disease; cancer;
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                                                                                                                                                                                                                                                                                                                                               WO200157271-A2.
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                     01-FEB-2002
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Gaps

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WO200157277-A2

ABA53200/c ID ABA53200 standard; DNA; 455 BP.

Query Match

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing grading, staging, monitoring and prognosing diseases of the human heart and vascular system
                                                                                                                                                                                                                                                                                                                                                                                                                        e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe #11347 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 455 BP; 104 A; 134 C; 129 G; 88 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.5%; Score 21.4; DB 22; 71.8%; Pred. No. 37; ive 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 tatttcccacccatatccccttgggcccttgggtgtgggg 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 TGTTTCCCACCCAATTCCCTAGCTCCACTGGGGGAGAG 52
                                                                                                                                                                                                                                         Claim 1; SEQ ID No 1442; 530pp; English
                                                                                                   Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rank DR;
                                                             (MOLE-) MOLECULAR DYNAMICS INC.
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-063366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234359.
04-OCT-2000; 2000GB-0024263.
                                                                                                   Chen W,
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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Best Local Similarity 71.8
Matches 28; Conservative
                                                                                                     Hanzel DK,
                                                                                                                                        WPI; 2001-488899/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe #1442 for gene expression analysis in human heart cell sample.
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                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; SEQ ID NO 14097; 639pp + sequence listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 TGTTTCCCACCCAAATTCCCTAGCTCCACTGGGGGAGAG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.5%; Score 21.4; DF 71.8%; Pred. No. 37; ive 0; Mismatches
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30-JUN-2000; 2000US-0668408.
03-AUG-2000; 2000US-052346.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234587.
04-OCT-2000; 2000GB-0024263.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
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ID ABA22976 standard; DNA; 455
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                                                        30-JAN-2001; 2001WO-US00669
                                                                                              2000US-0180312
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Matches 28; Conserv
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
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                  09-AUG-2001
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Length 455; Indels œ

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 455 BP; 104 A; 134 C; 129 G; 88 T; 0 other;
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                                                                                The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                       Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; brain expressed exon; gene expression analysis; probe; microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
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                                                                                                                                                                                                                                                                              Length 455;
                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                          Sequence 455 BP; 104 A; 134 C; 129 G; 88 T; 0 other;
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                                                                                                                                                                                                                                                                                                      0; Mismatches
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Pred. No. 37;
                                                         Claim 4; SEQ ID No 11347; 530pp; English.
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2000US-0608408.
2000US-0632366.
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2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epilepsy; cancer; ss
WPI; 2001-488899/53
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Best Local Similarity
Matches 28; Conserv
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human brains -
                                                                                                                                                             Gaps
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                                                                                                                  Length 455;
                                                                                                                                                             Indels
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                                           Sequence 455 BP; 104 A; 134 C; 129 G; 88 T; 0 other;
                                                                                                                                                           11;
                                                                                                                DB 22;
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                                                                                                             53.5%;
71.8%;
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2000US-0608408.
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                                                                                                      Query Match 53.5
Best Local Similarity 71.8
Matches 28; Conservative
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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30-JUN-2000;
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invention.
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DB 22; Length 455;

Score 21.4;

53.5%;

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(first entry)
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30-JUN-2000;
03-AUG-2000;
                                                                                                                                            Homo sapiens.
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               06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                            Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome-derived single exon nucleic acid probes useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 455;
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                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
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                                                                                                   90 TGTTTCCCACCCAAATTCCCTAGCTCCACTGGGGGAGAG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analyzing gene expression in human bone marrow
                                                                 2 tatttcccacccatatccccttgggcccttgggtgtggg
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Pred. No. 37;
0; Mismatches
           Pred. No. 37;
); Mismatches
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71.8%; Pre-
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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71.8%;
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         Best Local Similarity 71.8
Matches 28; Conservative
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21-SEP-2000;
27-SEP-2000;
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
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                                                               Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lynphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO: 14485; 658pp + Sequence Listing; English.
Human bone marrow expressed single exon probe SEQ ID NO: 14485.
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20000S-0236359.
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XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0232468.
PR 30-JUN-2000; 2000US-053236.
PR 21-SEP-2000; 2000US-0234687.
PR 21-SEP-2000; 2000US-0234687.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX WL-OCT-2000; 2000US-0236359.
PR A 4-OCT-2000; 2000US-0236359.
PR A 4-OCT-2000; 2000US-0236359.
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Best Local Similarity 71.8 Matches 28; Conservative

Query Match

g G Search completed: June 4, 2002, 17:56:22 Job time: 7110 sec

nucleic search, using sw model

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Run on:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_032802:*

Database

1736436 seqs, 858457221 residues

IDENTITY_NUC Gapoxt 1.0

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Ovine growth hormo
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  Fusarium venenatum
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             Propionibacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ligand; human cytomegalovirus; HCMY infection; herpetic ulcer; pneumonia; gastroenteritis; chorioretinitis; antiviral agent; herpesvirus infection; lesion; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA ligand #6 for human cytomegalovirus.
AAF09663
AAS5911
AAS51792
AAS61792
AAS61792
AAS61798
AAS677187
AAC6603
AAS67978
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4813
5351
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Synthetic.
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WO200138341-A1
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Human taste recept
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SIDS1/gcgdata/geneseq/genesegn-embl/NA1981.DAT:*
SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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                                                                                                                                                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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breast cance

SUMMARIES

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AAD10600 AAL11954

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Query Match Length DB

Score

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AAL20844 AAH17822

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650 2544 119 2687 3563 24813 2113

AAH33899 AAD17508 AAD17517 AAK70879 AAL26576

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Sequence 474 BP; 133 A; 118 C; 117 G; 104 T; 2 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            relates to human breast cancer expressed polynucleotides
Gaps
                                                                                     herpesvirus, particularly human cytomegalovirus (HCMV) to decrease or block HCMV infection in target cells. These ligands are used as anti-viral agents for the treatment of herpesvirus infections (e.g. lesions and herpetic ulcers) and particularly HCMV associated
                                                                                                                                         primary or chronic infections such as pneumonia, gastroenteritis and chorioretinitis. The present sequence is DNA ligand which bind to HCMV to decrease or block HCMV infection in target cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide useful as a marker for the diagnosis of breast cancer
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                                                                       to polynucleotide ligands which bind to
                                                                                                                                                                                                                                                Length 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human breast cancer expressed polynucleotide 4411.
                                                                                                                                                                                                                                                                                                      100.0%; Score 40; DB 22;
100.0%; Pred. No. 1.2e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                     Sequence 40 BP; 6 A; 12 C; 12 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; breast cancer; cell marker; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 797-798; 3695pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                         Page 6; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       AAL11954 standard; cDNA; 474
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2000US-0205230.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                             Ouery Match 100.
Best Local Similarity 100.
Matches 40; Conservative
                                                                      The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-451856/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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25-JUL-2000;
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24-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAL11954;
                                           Claim 8;
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                            Gaps
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    Length 474;
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                            Indels
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                                                                                                                                                                                                                          Human breast cancer expressed polynucleotide 13301.
                                                                                                                                                                                                                                                    Human; breast cancer; cell marker; cytostatic; ss.
    DB 22;
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                                                                             152 tetettaaaactagtetaeetaggetgggegtggtgg 188
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                                                      3 tcacttgaccctactctacctgggctggactgggtgg 39
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Pred. No. 13;
0; Mismatches
  22.6; I
No. 12;
                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 2357; 3695pp; English.
    Score
              Pred.
                                                                                                                                                ВР
                                                                                                                                             AAL20844 standard; cDNA; 650
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2000US-0193480.
2000US-0205230.
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 56.5%;
ilaxity 75.7%;
Conservative
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2000US-0220534
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Query Match
Best Local Similarity
Matches 28; Conserv
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les 28; Conser
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14 - MAR - 2000;
24 - MAR - 2000;
25 - MAY - 2000;
09 - JUN - 2000;
25 - JUL - 2000;
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                                                                                                                                                                       AAL20844;
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colon cancer; colon cancer antigen; diagnosis; detection;

colorectal carcinoma; ss.

Human;

WO200122920-A2 Homo sapiens.

05-APR-2001

Human colon cancer antigen encoding cDNA SEQ ID NO:955.

(first entry)

03-SEP-2001

AAH33899;

AAH33899 standard; cDNA; 119 BP

AAH33899

RESULT

RESULT

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonuclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nuclectide sequences defined in the specification, where the oligonuclectide comprising a sequence complementary to the complementary strand of a polynuclectide which comprises a 5'-end sequence and an oligonuclectide comprising a sequence complementary to a polynuclectide which comprises a 3'-end sequence. Where the oligonuclectide which comprises a 3'-end sequence to polynuclectide which comprises a 3'-end sequence where the oligonuclectide comprises a 3'-end sequence. The primer sets can be used in antisense therapy and the 5'-end sequence/3'-end sequence is selected from those defined in the section and/or in primers are useful for synthesising polynuclectides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs and the primers are also useful for AAH1362B and CAAH13633 to AAH13632B and cDNAs assally without any specialised methods. AAH03166 to AAH1362B and AAH16602.
                                                                                                                                                                                                                                                                                                                                                                                                         Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sogai T, Nishikawa T, Hayashi K, .Saito K, Ya
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2544 BP; 467 A; 775 C; 740 G; 562 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; SEQ ID 17492; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                             Human cDNA sequence SEQ ID NO:17492.
                                         AAH17822 standard; cDNA; 2544 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-1999; 99JP-0300253.
11-AAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-02418999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-2000; 2000EP-0116126.
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                                                                                                                                                                                                                           26-JUN-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                    AAH17822;
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AAH17822
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Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -

Rosen CA;

Birse CE,

Ruben SM, Barash SC, WPI; 2001-235357/24. P-PSDB; AAG74468

(HUMA-) HUMAN GENOME SCI INC

99US-0157137.

29-SEP-1999; 03-NOV-1999;

28-SEP-2000; 2000WO-US26524

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cancer-associated nucleic acid molecules (N) and proteins (P), where cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with decreased expression by rectifying mutations or deletions associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell of colorectal carcinomas and cancers. Administration, diagnosis and treatment of colorectal carcinomas and cancers. Administration of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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N.B. Pages 666 to 682 and page 7053 of the sequence listing were
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Pred. No. 36;
1; Mismatches
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SEQ ID NO:1027 to 1052, 7921 and 7922.
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72.2%;
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Best Local Similarity 72.29
Matches 26; Conservative
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ID AAD17
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6 cttgaccctactctacctgggctggactgggtggg 40

Score 22.2; DB.22; Length 2544; Pred. No. 22;

55.5%; 77.1%;

Best Local Similarity 77.1 Matches 27; Conservative

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Query Match

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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New mammalian taste-cell-specific G protein-coupled receptor polypeptides for identifying compounds that modulate taste signaling are useful in food, to modulate the sweet taste of foods or drugs
                                                         Human; taste-cell-specific G protein-coupled receptor; hTIR3; drug; genetic modulation; pharmaceutical; taste sensation; food industry; chemosensory transduction; chromosome 1p36.2-1p36.33; ds.
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                                          Human taste receptor, hT1R3 genomic DNA - 3' contig.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O'Connell SM,
                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0187546.
2000US-0195536.
2000US-0209840.
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2000US-0226448.
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/number= 4
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/number= 3
1300..1420
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848..961
                        10-DEC-2001 (first entry)
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2506..2687
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07-APR-2000;
06-JUN-2000;
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                                                                                              Homo sapiens
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17-AUG-2000;
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        AAD17508;
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modulate chemosensory transduction, such as taste sensation. The identification and isolation of movel taste receptors and taste signalling molecules allow for new methods of chemical and genetic modulation of taste transduction pathways. The taste modulating compounds are useful in pharmaceuticals and food industries to improve the tastes of a variety of consumer products, or to block undestrable tastes, e.g., in certain pharmaceuticals. TiR,s are also useful in biochemical assay for identifying tastent (TIR) ligands having binding specificity for TIR involved in taste signalling. The present sequence is human taste-cell specific G protein-coupled receptor, hills genomic DNA. 3° contig. Human TIR3 gene is localised on chromosome 1p36.2-1p36.33.
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; taste-cell-specific G.protein-coupled receptor; T1R3; drug; genetic modulation; pharmaceutical; taste sensation; food industry; chemosensory transduction; chromosome 1p36.2-1p36.33; ds.
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/product= "Human taste receptor, hTIR3 protein"
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                                                                                                                                                                                                                   Length 2687;
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                                                                                                                                                                       Sequence 2687 BP; 403 A; 920 C; 885 G; 479 T; 0 other;
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211..401
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human taste receptor, hT1R3 full-length genomic DNA.
                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                          52.0%; Score 20.8; Cilarity 70.0%; Pred. No. 80; Conservative 0; Mismatches
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ID AAD17517 standard; DNA; 3563 BP
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/number= 5
2176..2296
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2042..2175
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/*tag= b
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/*tag= f
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Best Local Similarity
Matches 28; Conserv
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Human; immune; haematopoletic; immune/haematopoletic antigen; cancer;
           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25691.
                                          cytostatic; gene therapy; vaccine; metastasis; ds.
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2000US-0205515
                                                                                                                             17-JAN-2001; 2001WO-US01354
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                                                                Homo sapiens
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08-SEP-2000;
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14-SEP-2000;
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14-AUG-2000;
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                                                                                                        09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to mammalian taste-cell-specific G protein-coupled receptors, TIR and their corresponding cDNA molecules. Taste receptors, TIR are useful for screening compounds which are used to activate or modulate chemosensory transduction, such as taste sensation. The identification and isolation of novel taste receptors and taste signalling molecules allow for new methods of chemical and genetic modulation of taste transduction pathways. The taste modulating compounds are useful in pharmaceuticals and food industries to improve the taste of a variety of consumer products, or to block undesirable tastes, e.g., in certain pharmaceuticals. TIR, a are also useful in specificity for TIR involved in taste signalling. The present: sequence is human taste-cell-specific G protein-coupled receptor, hTIR3 full-length genomic DNA. Human TIR3 gene is localised on chromosome 1p36.2-1p36.33.
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                                                                                                                                                                                                                                                                                                                                                       New mammalian taste-cell-specific G protein-coupled receptor polypeptides for identifying compounds that modulate taste signaling are useful in food, to modulate the sweet taste of foods or drugs -
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Pred. No. 83;
0; Mismatches 12; Indels 0;
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                                                                                                                   'cons_splice (5'site:NO, 3'site:NO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK70879 standard; DNA; 24813 BP
                                                                                                                                                                                                                2000US-0195536.
2000US-0209840.
2000US-0214213.
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Best Local Similarity 70.0%;
Matches 28; Conservative (
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03-JAN-2001; 2001US-025927.
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/*tag= k
/number= 5
2297..2422
/*tag= 1
/number= 6
                                                  2423..3381
/*tag= m
/number= 6
3382..3563
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                                                                                                       'number-
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P-PSDB; AAE10366.
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06-JUN-2000;
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2000US-0249208.
2000US-0249209.
2000US-0249210.
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2000US-0249216.
2000US-0249217.
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2000US-0249265.
2000US-0249297.
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2000US-0249245.
             2000US-0235834
                                                       2000US-0236367
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2000US-0251869
2000US-0235484
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08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
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7-NOV-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) and acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome cappelement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent.

C diagnose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoletic antigen genomic capresent human immune/haematopoletic antigen genomic sequences from the present invention. AAK84942 to AAK84950 and AAM82169 cepresent invention. AAK84942 to AAK84950 and AAM82169
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                                                                                                                                                                                      Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 25691; 3071pp + Sequence Listing; English.
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AAL26576/c
TD AAL26576 standard; cDNA; 2113 BP.
                                                                                                                     Ruben SM;
                                                                                   (HUMA-) HUMAN GENOME SCI INC.
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2000US-0189167.
2000US-0192099.
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2000US-0205230.
2000US-0211315.
               08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
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Best Local Similarity 78.1<sup>§</sup>
Matches 25; Conservative
                                                                                                                   Rosen CA, Barash SC,
                                                                                                                                                   WPI; 2001-483436/52.
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15-MAY-2000;
09-JUN-2000;
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24-MAR-2000;
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                                                                                                                                                                                                                          metastasis
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CC The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes from FF cells allows the production of phosis from FF cells allows the production of potential of the microorganisms to be improved. New genes may be consible functions of unknown open reading frames can be discovered, possible functions of unknown open reading frames can be discovered, possible functions of unknown open reading frames can be discovered, possible functions of unknown open reading frames can be discovered. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore contineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an example of the results. AAF01247 represents ESTs from Aspergillus or Marcarays based on function of the gene products to facilitate analysis of the results. AAF01248 to AAF11247 represents ESTs from AAF1289 to AAF1289 to AAF1287 from AAF14879 to AAF1287 from AAF14879 to AAF1337 represents ESTs from AAF14879 to AAF15337 represents ESTs from AAF14879 to AAF15337 represents ESTS from AAF14879 to AAF154879 to AAF154879 to AAF154879 to AAF154879 to AAF154879 to AAF154876 multiproducts in the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 615;
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Jen S, Carter D;
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0; Mismatches
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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e J, Zhang Y,
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Matches 27; Conserv
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                                                                                                                                                                                                                                                                                                                                             (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesel; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                        invention relates to human breast cancer expressed polynucleotides
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                                                                                                                                                                                                                  New peptide useful as a marker for the diagnosis of breast cancer
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                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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Pred. No. 93;
                                                                                                                                                                                                                                                                      Claim 1; Page 3573-3574; 3695pp; English.
                                                                                                                Steinmann K;
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74.3%;
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                                                                                                             Xu Y, Wang Y,
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                                                                                                                                                              WPI; 2001-451856/48
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Best Local Similarity
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                                                                                                          Lillie J,
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29-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 51.0%; Score 20.4; DB 23; Best Local Similarity 71.1%; Pred. No. 1.6e+02; Matches 27; Conservative 0; Mismatches 11;
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                                     Claim 1; SEQ ID No 6; 1069pp; English.
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2000US-0189874.
2000US-0190076.
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2000US-0205515.
2000US-0209467.
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2000US-0217487
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   treating acne vulgaris
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16-MAR-2000;
17-MAR-2000;
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19-MAY-2000;
07-JUN-2000;
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AAK81665/c
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amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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                                                              2000US-0246478.
2000US-0246523.
2000US-0246524.
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17-NOV-2000,
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08-DEC-2000;
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protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huntingtin Interacting Protein; HIP; death effector domain; DED; human; apotosis; HIP-apoptosis modulating protein; cell death; gene therapy; Huntington's disease; nootropic; anticonvulsant; cytostatic; exon;
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DM;
                                                                                                                                                                                                                                                  Sequence 24908 BP; 6781 A; 4773 C; 5094 G; 8260 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                 Score 20.4; DB 25
Pred. No. 1.6e+02;
0; Mismatches 11
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(MERI ) MERCK FROSST CANADA INC
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Best Local Similarity 71.1%;
Matches 27; Conservative
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JP, Rasper
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Conservative

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Matches

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The invention relates to novel isolated lung small cell cancer antigen

Cancer in a patient. The method is optionally performed by

cancer in a patient. The method is optionally performed by

utilising oligonucleotides (III), where the biological sample

C from the patient is contacted with (III), detecting the amount of

polynucleotide hybridised to (III) in the sample and comparing the

amount of polynucleotide to a predetermined cut-off value and thereby

determining cancer in a patient. (II), (II) or antigen-presenting cells

c specific for a tumour protein. The method comprises contacting T cells

c specific for a tumour protein. The method comprises contacting T cells

c with one of the components under conditions to permit the stimulation

and/or expansion of the cells. A composition comprising (I) is useful for

stimulating an immune response in a patient and for inhibiting the

development of a cancer especially lung cancer in a patient. An

c isolated T cell population is useful for removing tumour cells from the

blological sample and for inhibiting the development of cancer in a

contact in a patient. Ansight of the cells of the component of cancer in a patient. Ansight of the cells of the cells. According the cells of the cells. According the cells of the cells. According the cells of the cells. According the cells of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytostatic; antitumour; lung small cell cancer antigen;
       Length 359;
                                                       Indels
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       21;
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Score 20.2; DB 2
Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                  Lung small cell carcinoma antigen, cDNA #333
                                                0; Mismatches
                                                                                                                        188 TCTCTCGTTCCAAATCTACCTGGGCTTGTCTGG 156
                                                                                              3 tcacttgaccctactctacctgggctggactgg
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2000US-213361P.
2000US-229763P.
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2000US-232565P.
2000US-257037P.
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  50.5%;
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                                                25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour; lung cancer; ss.
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05-SEP-2000;
14-SEP-2000;
19-DEC-2000;
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21-JUN-2000;
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                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A cDNA clone (AAT67186) codes for a portion (AAM18029) of huntingtin interacting protein HIP1, a brain-specific protein that interacts differently with the gene product of a normal (16 CAG repeat) and an expanded (ever 44 CAG repeat) Huntington's disease (HD) gene. It was isolated from a yeast two-hybrid screen utilising an adult human brain cDNA library. Further screening of a frontal cortex cDNA library and 5' RACE yielded a longer portion (AAT67187) of the 10 kb HIP1 message that had a coding sequence for a 914-amino acid protein (AAM18030). HIP1 maps to 7411.2 Gene therapy can be used to increase expression of HIP1 as a means of ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pathology in patients expressing huntingtin with expanded polyglutamine tracts. Probes can be used to localise and quantify the presence of HIP-1 nucleic acids.
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                                                                                                                                                                                                                                            Huntingtin interacting protein; HIP1; Huntington's disease; gene therapy; diagnosis; ss.
                                                                                                                                                                                                             Huntingtin interacting protein HIP1 cDNA partial sequence.
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778 TCTCTCGTTCCAAATCTACCTGGGCTTGTCTGG 746
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                                                                                               AAT67186/c
ID AAT67186 standard; cDNA; 1164
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Best Local Similarity
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Search completed: June 4, 2002, 17:56:19

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Score 20.2; DB 24; Length 601; Pred. No. 1.1e+02;

50.5%;

Query Match Best Local Similarity

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El-Sayed, N.M., Ghedin, E., Song, J., Larkin, C., Wanless, D., Jones, K., Peterson, J., Hou, L., Zhao, H., Mason, T., Militscher, J., Pai, G., Van Aken, S., Utterback, T., Khalak, H.G., Gerard, C., Leech, V., Ullu, E., Melville, S., White, O., Adams, M.D., Donelson, J.E. and Fraser, C.M. Trypanosoma brucel GUTatlo.1 RPC193-29M18 BAC genomic sequence
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B1-SaydA N.W. Khalak,H. and Adams,M.D.
Direct Submission
Submitted (25-DEC-2000) The Institute for Genomic Research, 9712
                                                Homo sap
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AC023107 H
AC013272 H
AL355974 H
AL355987 H
AC080508 M
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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romosome IV clone RPCI93-29M18,
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                      1797656 seqs, 10463268293 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cosmid R28194 overlaps cosmid R31546 to the left and R28550 to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
By Startens Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 40649)
Lamerdin, J.E., McCready, P.M., Adamson, A.W., Burkhart-Schultz, K., Gordon, L., Christensen, M., Kyle, A., Ramirez, M., Stilwagen, S., Garnes, J., Danganan, L., Brucce, R., Quan, G., Montgomery, M., Ow, D., Scquence, analysis of an OLFR cluster in 19913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (21-NOV-1997) Human Genome Center, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from p telomere to centromere.
             on Jul 17, 201 this sequence version replaced gi:13277449.

**NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs a rare represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

**This sequence will be replaced

**This sequence will be replaced

**This sequence as soon as it is available and

**The finished sequence as soon as it is available and

**The accession number will be preserved.

**Institution of 125817 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="LL19NCO3 R chromosome 19 specific cosmid library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACOU3111 40649 bp DNA linear PRI 21-NC Human DNA from chromosome 19-specific cosmid R2B194, genomic sequence, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 125817;
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Medical Center Dr, Rockville, MD 20850, USA
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/map="19913 from OLFR to D19511"
/clone="R28194"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                    1. .125817
/organism="Trypanosoma brucei"
/isolate="GUTat10.1"
                                                                                                                                                                                                                                                                                                                                                                                                /clone="RPC193-29M18"
33614 a 30508 c 27770 g 33925 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 60.5%; Score 24.2; D
Best Local Similarity 78.4%; Pred. No. 6.8;
Matches 29; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:5691"
/chromosome="IV"
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ACO03111.1 GI:2636670
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KEYWORDS
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-region complement(18, 51)

-region complement(18, 21)

-region complement(18, 2086)

-region complement
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Db 39928 TCACTGCACCAATCTCTAGCTGGGCTGGACAGGGT 39962
                                                                                             RESULT 3
AC004798/c
LOCUS
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3255. 33034

700te-"predicted exon, program; grail2exons_human_1.3, frame: 1, quality; good, score: 74.000-(33133. 32791) DDS slmilarity to M78531 EST00679 Homo sapiens cDNA clone HFRCD86. Score: 675 Identity: 342/344 (99%)."

Complement(3310. 33297)

/rpt_family="Alu"
33955. 33753

/note-"predicted exon, program; grail2exons_human_1.3, frame: 0, quality; good, score: 55.000"

/rpt_family="Alu"
339577. 34060)
20057. .20709
//occe="Overlapping EST matches:
//occe="Overlapping EST matches:
//occe="Overlapping EST matches:
//occe="Overlapping EST matches:
//occes fetal liver spleen lNFLS SI Homo sapiens cDNA clone
//occes fetal liver spleen lNFLS SI Homo sapiens
//occes 465 Identity: 271/294
//occes 465 Identity: 271/294
//occes 645 Identity to AA004397
//occes 6461 liver spleen lNFLS SI Homo sapiens
//occes 697 Identity: 427/467
//occes 697 Identity: 427/467
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Homo sapiens cDNA clone 683031 5'. Score: 932 Identity:
494/507 (97%)."
                                                                                                                                                                                                                     complement(22031. .22293)
/rpt_family="Alu"
complement(22105. .22192)
/rote="predicted exon, program: grail2exons_human_l.3,
frame: 2, quality: excellent, score: 95.000"
complement(23167. .23252)
23515. .23793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(25990. .26238)

/rpt_family="Alu"

/rpt_family="Alu"

/rpt_family="Alu"

/note="predicted exon, program: grail2exons_human_1.3,

/note="predicted exon, program: grail2exons_human_1.3,

/rote=family="Alu"

/rpt_family="Alu"

/rpt_family="Alu"

/rpt_family="Alu"

32439. .32733
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36686 .36726
/note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 80.000"
complement(38428. 38928)
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/rpt_family="Alu"
24722. .24781
/rpt_family="MER3"
25041. .25102
/rpt_family="MER33"
                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="Alu"
24039. .24159
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32925. 3307
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ORIGIN
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Indicate Cosmid library constructed at LLNL from flow-sorted chromosomes from hybrid HL2-B, which carries chromosome 19 as 1ts only human chromosome."

Topt_family="AluSx" | 10.24

/rot_family="AluSx" | 10.24

/rote="DDS similarity to overlapping ESTS: (455. .714) T51949 yb29803.s1 Homo sapiens cDNA clone 72556 3'; Score: 452 Identity: 247/270 (91%). (1024. .669) T52030 yb29803.s1 Homo sapiens cDNA clone 72556 5'; Score: 615 Identity: 351/367 (95%)."

//rote="DDS similarity to overlapping ESTS: (1774. .2133 //rote="DDS similarity to overlapping ESTS: (1774. .2177) N23663 yw40bl0.s1 Homo sapiens cDNA clone 254683 3'. Score: 741 Identity: 399/407 (98%). (1774. .2177) MAG45513 na21h09: s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184321 similar to contains element ITR4 repetitive element; Score: 812 Identity: 431,232,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1771. .2333) AA534457 nf80d06.s1 NCI_CGAP_CO3 Homo saplens
CDNA clone IMAGE:926219; Score: 1019 Identity: 542/568
AC004798 42497 bp DNA linear PRI 05-JUN-1998
Homo sapiens chromosome 19, cosmid R31546, complete sequence.
AC004798
                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I bases I to 42497)

Lamerdin, J.E., McCready, P.M., Skowronski, E., Adamson, A.W.,

Burkhart-Schultz, K.J., Gordon, L., Kyle, A., Ramirez, M.,

Stlwagen, S., Phan, H., Velasco, M., Do, L., Regala, W., Terry, A.,

Garnes, J., Danganan, L., Poundstone, P., Christensen, M.,

Georgescu, A., Avila, J., Liu, S., Attix, C., Andreise, T.,

Bruce, R., Thomas, P., Quan, G., Kronmiller, B., Arellano, A.,

Montgomery, M., Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1776. .2180) AA278745 zs79912.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703750 3'; Score: 781 Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_line="5HL2-B"
/clone_lib="LL19NC03 R chromosome 19 specific cosmid
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence analysis of an ~1.5 Mb OLFR cluster in 19p13.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131/438 (98%).
                                                                                     AC004798.1 GI:3184497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 42497)
Lamerdin, J.E.
Direct Submission
                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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AUTHORS
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JOURNAL
                                                              ACCESSION
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KEYWORDS
SOURCE
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Gaps

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7;

Score 23.8; DE Pred. No. 10; 0; Mismatches

59.5%; 80.0%;

Query Match 59.5 Best Local Similarity 80.0 Matches 28; Conservative

DB 9; Length 40649; Indels

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/gene- noun.
//gene- noun.
//g
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| (12541. .12067) | A4429349 zv50091.sl Score: 809 Identity: 41377 (96%).
| (12197. .12067) | A4429349 zv50091.sl Score: 978 Identity: 495/501 (98%).
| (12197. .1202) | AA29149 zv50091.sl Score: 978 Identity: 495/501 (98%).
| (12197. .1202) | AA29140 zv188f02.sl Score: 978 Identity: 500/506 (98%).
| (12880. .12348) | M45196 yz14all.sl Homo sapiens CDNA clone 1283004 3; Score: 1068 Identity: 573/584 (98%).
| (12880. .12348) | A4625129 af70a09.rl Score: 1017 Identity: 527/528 (99%).
| (13237. .12768) | AA291565 zt38f02.rl Score: 895 Identity: 466/469 (99%).
| (13237. .1286) | AA29161 zv50901.rl Scores ovary tumor NDHOT Homo sapiens CDNA clone 724635 5'; Score: 895 Identity: 466/469 (99%).
| (13237. .12850) | AA428761 zv50901.rl Scores ovary tumor NDHOT Homo sapiens CDNA clone 757104 5'; Score: 776 Identity: 388/388 (100%).-Other overlapping EST matches: refined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC109621/c
LOCUS AC109621 45420 bp DNA linear HTG 06-FEB-2002
DEFINITION Mus musculus clone RP23-330J17, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1/5/0. .18018
//note="books similarity to AA262797 zs24f07.r1 NCI_CGAP_GCB1 Home subbs similarity to AA262797 zs24f07.r1 NCI_CGAP_GCB1 Home subbens cone image: 686149 5'; Score: 833 Identity: 435/446 (97%)."
complement(18294. .18623)
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/gene="HUNK1"
/product="H. sapiens HUNK1 (Y12059)"
/complement(13455. .>38069)
/gene="HUNK1"
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/rpt_family="(CAGA)n"
complement(10070. .10174)
/rpt_family="MIR"
11994. .13585
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80.0%; Pred. No. 10;
iive 0; Mismatches
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/gene="HUNK1"
                              Identity: 236/255 (928"
                                                                 9400. .9540
/rpt_family="(TGG)n"
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Best Local Similarity 80.0°
Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (2345. 2777) AA121152 z188e01.51 Stratagene colon (#937204) Homo sapiens cDNA clone 511704 3'; Score: 842 Identity: 430/433 (998).
(3003. 2614) AA121132 z188e01.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 511704 5'; Score: 726 Identity: 383/386 (998).
(2496. 2807) T0/432 EST05321 Homo sapiens cDNA clone HFBE195; Score: 565 Identity: 306/317 (968).
(2950. 2560) R68397 yh99h03.r1 Homo sapiens cDNA clone 137909 5'. Score: 687 Identity: 382/396 (968).
(3073. 2821) T8539 yd78h03.r1 Homo sapiens cDNA clone 114389 5'. Score: 463 Identity: 24/254 (968).
(2055. 2902) AA666963 W186406.51 Knowles Solter mouse 2 cell Mus musculus cDNA clone 1135595 5'; (355. 514) 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (2342. .2769) AA579808 nk43f03.s1 NCI_CGAP_GC2 Homo sapiens CDNA clone IMAGE:1016285; Score: 848 Identity: 426/428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complement(3776. .3858)
/ Trpt_family="Polity_A"

complement(3776. .3858)
/ Trpt_family="(CAG)"
/ Trpt_family="(CAG)"

complement(4402. .4458)
/ Trote="DDS similarity to AA666963 vr86d06.sl Knowles
Solter mouse 2 cell Mus musculus cDNA clone 1135595 5;
(298. .354) 88% identity."

complement(4565. .4757)
/ Note="DDS similarity to AA666963 vr86d06.sl Knowles
Solter mouse 2 cell Mus musculus cDNA clone 1135595 5;
(135. .297) 86% identity."

complement(4846. .4973)
/ Note="DDS similarity to AA666963 vr86d06.sl Knowles
Solter mouse 2 cell Mus musculus cDNA clone 1135595 5;
(11. .134) 84% identity."
/ Solver mouse 2 cell Mus musculus cDNA clone 1135595 5;
(12. .344) 84% identity."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(8151. '8405)
Anote-"DDS similarity to AA057523 zf56e09.rl Soares retina NZD4HR Homo appiens CDNA clone 380968 5' similar to contains element MSR1 repetitive element; Score: 434
402/404 (99%).
(1800. .2152) R34240 yh80f09.s1 Homo sapiens cDNA clone 136073 s similar to conteains TARI repetitive element; Score: 614 Identity: 346/363 (95%).
(2249. .1897) IN71602 yw40b10.r1 Homo sapiens cDNA clone 254683 5' similar to contains element MER6 repetitive element; Score: 588 Identity: 335/357 (93%).
(2212. .1967) AA304414 EST16821 Aorta endothelial cells, TNF alpha-treated Homo sapiens cDNA 5' end; Score: 443 Identity: 238/255 (93%).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (6747. 7049)
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/rpt_family="(TGG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'rpt_family="MER5A"
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2342.
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Gaps

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100 bp f 709 bp in length

contig of

in length

of 100 bp contig of 714 bp 685

100 100

contig of

bp in length

contig of 660 100

: gap 6291: : gap 7098:

6391: 5631;

contig of 707 bp in length

, bp S bp 3

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9796 9506: control of 700 bp in length 10318 10417: control of 711 bp in length 10318 10417: control of 711 bp in length 10318 10417: gap of 100 bp 10418 11109: gap of 100 bp 11200 11999: gap of 100 bp 11200 11999: gap of 100 bp in length 11210 12099: gap of 100 bp in length 12710 12809: gap of 100 bp in length 13509: control of 691 bp in length 13509: gap of 100 bp in length 13509: gap of 100 bp in length 1400 14299: gap of 100 bp in length 1400 15105: control of 700 bp in length 1500 15009: gap of 100 bp in length 15209: control of 705 bp in length 15209: gap of 100 bp in length 15209: control of 700 bp in length 1521 1622: gap of 100 bp in length 1523 1622: gap of 100 bp in length 1523 1622: gap of 100 bp in length 1520 19099: control of 704 bp in length 19000: gap of 100 bp in length 20000: gap of 100 bp in length 200000: gap of 100 bp in length 20000: gap of 100 bp in length 200000
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                                                                                                      7198: gap (
                                                                                                                                                          7983: gap c
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20800
21509
21609
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7199
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7984
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25592
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26355
27059
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32671
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                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (06-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This record contains 57 individual

* sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 753: contig of 753 bp in length 754 853: gap of 100 bp 854 1553: contig of 700 bp in length 1554 1653: gap of 100 bp 1654 2333: contig of 680 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1653: gap of 100 bp
2333: contig of 680 bp in length
2433: gap of 100 bp
3164: contig of 731 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of 703 bp in length of 100 bp contig of 705 bp in length of 100 bp
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                                                                                                                                                                          1 (bases I to 45420)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-330J17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ф
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  AC109621
AC109621.1 GI:18543039
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3967: co
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4772: co
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                                                    HTG; HTGS_PHASE0
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                                                                                                           Mus musculus
                                                                                                                                                                                                                                                            Unpublished
                                                                              house mouse
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22434
3165
3265
3968
4773
4873
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
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27035 Cont.19 of 704 bp in length 27861; contig of 703 bp in length 1961; gap of 100 bp 28665; contig of 705 bp in length 29666; gap of 100 bp 29476; contig of 710 bp in length 19576; gap of 100 bp 100 bp 130272; contig of 696 bp in length 1367; contig of 690 bp in length 1162; gap of 100 bp 100 bp 1162; gap of 100 bp 1162; gap of 100 bp 11643; gap of 100 bp 100 bp 11670; gap of 100 bp 100 bp 11670; gap of 100 bp 100 bp 116710; gap of 100 bp 100 bp 116710; gap of 100 bp 100 bp 116710; gap of 100 bp 10

31162: 31967: 32770: 33575:

30372

29576: gap of

28766: gap of

27158: 27961:

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Direct Submission

Direct Submission

Buren, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (Dasses I to 157076)

Buren, B. Lintcon, L. Nusbaum, C., Lander, E., Alli, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Cahang, J., Chargor, C., Chang, J., Chargor, C., Chang, J., Chargor, B., Chang, J., Changor, C., Chang, J., Chargor, B., Chock, P., Cock, P., Collins, S., Collymore, A., Cook, A., Cook, P., Devar, K., Diaz, J.S., Dodge, S., Faro, S., Fitzkugh, W., Gago, C., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Gardyna, S., Gord, S., Goyette, M., Graham, L., Gardyna, S., Liu, G., Maccan, A., Horton, L., Hulme, W., Illey, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Marquis, N., Matthews, C., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., Maccan, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Nacdonald, P., Major, J., Marquis, N., Matthews, C., Nacdonald, P., Major, J., Marquis, N., Matthews, C., Ramat, A., Keback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Nell, D., O'Liver, J., Peterson, K., Phunkhang, P., Pierre, N., Schupback, R., Schauer, S., Severti, M., Roy, A., Santos, R., Schupback, R., Schauer, S., Severti, M., Roy, A., Santos, R., Schauer, S., Treoder, J., Vo, A., Wilson, B., Travis, N., Travis, N., Yew, J., Vo, A., Wilson, B., Yuwan, D., Ye, W.J., Yo, A., Wilson, B., Yuwan, D., Ye, W.J., Yo, A., Wilson, B., Wunan, D., Ye, W.J., Yo, A., Wilson, B., Wunan, D., Ye, W.J., Yo, A., Wilson, B., Zoll this sequence version replaced gi:16041469.

All repeats were identified using Repeatmasker: hml

Conter: North C., Connor, Conno
Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Petersor, P. Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Stoy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stoyanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell. A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP11-563019"
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8. .2498
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Web site: http://www-seq.wi.mit.edu
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Center project name: L4200
Center clone name: 563_0_19
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/rpt_family-"MLTIG"
3288. .3810
/rpt_family-"MLTIFI"
3846. .4155
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7069. .7096
/rpt_family-"AT_rich"
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/rpt_family="LlMB4"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 157076)
Birran, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 8, clone RP11-563019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC019031 157076 bp DNA linear PRI 01-DEC-20
Homo saplens chromosome 8, clone RP11-563019, complete sequence.
AC019031
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8360 c 8491 g 11360 t 6196 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39806 39905: gap of 100 bp 100
                                                                                                 3: gap of 100 bp 100 bp
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43823: contig of 713 bp in length
23: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                       contig of 668 bp in length p of 100 bp contig of 699 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43824 43923: gap of 100 bp
43924 44627: contig of 704 bp in length
35109: contig of 720 bp in length
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44728 45420: contig of 693 bp
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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                                                                          contig of
                                                                                                                                                                            36690 36789: gap of
36790 37484: contig
                                                                                                                                                                                                                                                                                                                                                                                                          39106: gap of
39805: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39806 39905: gap of
39906 40618: con
                                                                                                     35909 36008; gap of
36009 36689; con
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43011 43110: gap of
                                   5110 35209: gap of
5210 35908: con
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Best Local Similarity 79.47
Matches 27; Conservative
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12363. 12426
/rpt_family="MER116"
/rpt_family="MER116"
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24572. .2487
24692. .2477
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32393. .32967
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omplement/locations
                                                                                                                                                                                               /rpt_family="MER105"
complement'14"
                                                                                                                                                                                                                        /rpt_family="MER3" .14569)
[5351. .15370
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/rpt_family="AluJb"
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12832. 12915

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14144. 14185

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complement(14195. 1428
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/rpt_family="MIR"

/rpt_family="MIR"

/rpt_family="AIR"

/rpt_family="AI_rich"

19046. 19409
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complement(28357. .28t
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10359. .10847
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22347. .22531
/rpt_family="AluJo"
22560. .23596
23589. .24051
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21139. .22344
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complement(24225. .2
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10410. .20599
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 212671)

Mupublished

Z (bases 1 to 212671)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastien, V., Beda, F., Bougalavkiy, L., Burne, N., Bastien, V., Beda, F., Bougalavkiy, L., Burne, D., Collymore, A., Cocke, P., Dohepel, Y., Colangelo, M., Collins, S., Collymore, A., Cocke, P., DeArellano, K., DeWar, K., Dida, J.S., Dodge, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagn, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Lieu, C., Liu, G. Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollvar, T. M., Ollver, J., Peterson, K., Forbumen, D., Roy, A., Santos, R., Schauer, S., Severy, P., Sougnez, C., Spencer, B., Stalamas, J., Tesfaye, S., Theodore, J.,
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3316. 33467
/rpt_family="MER2"
complement(33468. 33758)
/rpt_family="AluSq"
33759. 33964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 57.0%; Score 22.8; D
Best Local Similarity 79.4%; Pred. No. 28;
Matches 27; Conservative 0; Mismatches
                                                                                                                              33759. .33964
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complement(33996. .34173)
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34955. .34982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="HAL1"
complement(38721, .38883)
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39259, .39448
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/rpt_family="HALI"
37160. .37460
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/rpt_family="HALI"
38194. .38491
/rpt_family="HALI"
38192. .38492
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35990. .36115
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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/rpt_family="L2"
36267. acad
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0 212671: contig of 552 bp in length. Location/Qualiflers

212120

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RESULT 7
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Tirrell, A., Travers, M., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Dirnect Submission
Submitted (22-NOV-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washingcon.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                      ...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                              Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project information
Center project name: 111002
Center clone name: 460_1_20
Center clone name: 460_1_20
Center clone name: 460_1_20
Center clone name: 5001120
Center clone name: 460_1_20
Center clone name: 460_1_20
Center project name; 503142 bases at least 030
Consensus quality: 20876 bases at least 030
Consensus quality: 20876 bases at least 030
Consensus quality: 209766 bases at least 030
Consensus quality: 509000; sqarose-fp
Insert size: 200000; sqarose-fp
Ouality coverage: 5.9 in Q20 bases; sum-of-contigs
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62134: contig of 4513 bp in length
34: gap of 100 bp
69724: contig of 7490 bp in length
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41448 42786: contig of 1339 bp in length
42787 42886: gap of 100 bp
43897: contig of 1009 bp in length
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15381 46855: contig of 1475 bp in length
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77605: contig of 7781 bp in length
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40695 41347: contig of 653 bp in length
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104044; ~
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54861: cont
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ACU91573

Linear HTG 11-FEB-2002

Homo sapiens chromosome 8 clone RP11-420F14 map 8, *** SEQUENCING
IN PROGRESS ***, 3 unordered pieces.
AC091573

RC091573.7 GI:18464127

HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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79.4%; Pred. No. 28;
ive 0; Mismatches 7; Indels 0;
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                                                                                        /clone="RP11-460120"
/clone_lib="RPCI-11 Human Male BAC"
1. .40594
/note="assembly_fragment
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48980 c 50176 g 55186 t
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45381 .46855
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46956 .48506
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48607 .52429
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52530 .54861
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54962 .57521
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43996. .45280
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88791. .104044
1. .212671
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/db_xref="taxon:9606"
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40695. .41347
                                                        /chromosome="8"
                                                                                                                                                                 clone_end: SP6
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Best Local Similarity 79.4%;
Matches 27; Conservative
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57.0%; Score 22.8; DB 9; Length 213621;
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Contact: sequence_submissions@genome.wi.mit.edu
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Unpublished
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50973 c 49786 g 54679 t 200
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Pred. No. 28;
0; Mismatches
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/db_xref="taxon:9606"
/chromosome="8"
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Matches 27; Conservative
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AF276759 213621 bp DNA linear PRI 06-FEB-2002
Homo sapiens chromosome 8 clone RP11-420F14 map 8p12, complete
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 213621)
Wen,G., Reichwald,K., Baumgart,C., Taudin,S., Baumgart,C. and Platzer,M.
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Direct Submission

Sub
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Web site: http://genome.imb-jena.de/
Contact: gscj-submitégenome.imb-jena.de/
Contact: gscj-submitégenome.imb-jena.de/
Contact: gscj-submitégenome.imb-jena.de/
Contact: gscj-submitégenome.imb-jena.de/
Center project name: H5134

Center project name: H5134

Center clone name: H7134

Center clone name: H7134

Center project name: H7134

Consensus quality: 206055 bases at least Q40

Consensus quality: 208130 bases at least Q30

Consensus quality: 2081300 bases at least Q20

Quality coverage: 4.63 x in Q20 bases; sum-of-contigs
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All manually edited bases have been reduced to quality Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
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HTG: HTGS_FULLTOP; HTGS_ACTIVEFIN

    213621
    organism="Homo sapiens"

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Unpublished
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Rattus

Rattus
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Rattus norvegicus clone CH230-99H20, *** SEQUENCING IN PROGRESS
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                             Gaps
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On Jan 10, 2002 this sequence version replaced gi:17973191.
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HTG; HTGS_PHASE1.
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 58 contigs. The true order of the pieces is not known and their order in this sequence record is abbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                    Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 0.9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                         * NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                          Consensus quality: 86652 bases at least Q40 Consensus quality: 94918 bases at least Q30 Consensus quality: 101775 bases at least Q20 Estimated insert size: 84769; sum-of-contigs estimation
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                                                                                                        -------- Summary Statistics
Assembly program: Phrap; version 0.990329First call
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Web site: http://www.hgsc.bcm.tmc.cdu/
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                                        Center project Information
Center project name: GHJA
Center clone name: CH230-99H20
                     Contact: hgsc-help@bcm.tmc.edu
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length

unknown

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ALL Submitted (13-NOW-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: hunguery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
hunguery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
nunguery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 10, constructed by the Sanger Centre Chromosome 10
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chrl0
This sequence is the entire insert of clone RP11-264E18 The true
left end of clone RP11-41F2:5 is at 67259 in this sequence. The
true left end of clone RP11-36A2 is at 47064 in this
sequence: This sequence was finished as follows unless otherwise
noted: all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (1.e., phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one Mi3
subclone; and the assembly was confirmed by restriction digest.
RF11-264E18 is from the library RR21-11.1 constructed by the group
there is a seambly was confirmed by the set of pieter de Jong, For firther details see
                                                AL390763 162044 bp DNA linear PRI 03-DEC-2001
Human DNA sequence from clone RPI1-264E18 on chromosome 10,
                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 162044)
Whitehead, S.
Direct Submission
Submitted (13-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
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561. .799
/note="LIMEc repeat: matches 2260. .2140 of consensus"
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/clone_lib="RPCI-11.1"
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/note="match: GSS: Em:AQ486326"
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/note="match: GSS: Em:AQ487135"
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VECTOR: pBACe3.6.
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/organism="Homo sapiens"
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1278. .1440 /note="LTR16A repeat: matches 23. .193 of consensus"

repeat_region

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1441. .1498 /note="2 copies 29 mer 98% conserved" repeat_region

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/note="Sequence from overlapping clone AL358092. Assembly confirmed by restriction digest" 1739.\ .1840
                                                                                                                                                                    23371. 24290

/note="46 copies 20 mer 83% conserved"

24399. 24639

25098. 25157
                                                                                     /note="MER91c repeat: matches 1. .108 of consensus"
3406. .3717
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                                                                                                               3406. 3717 repeat: matches 1. .108 of consensu nnote-"Alux repeat: matches 1. .311 of consensus" 1723. .3746
                                                                                                                                                                                                                                                                            1737. .4882
//note="MIR repeat: matches 19. .182 of consensus"
1995. .5460
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5165. .25500
note="MER2 repeat: matches 4. .343 of consensus"
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AC023276 11 nordered pieces.

AC023276 DNA 11near HTG 07-JUL-2000 SEQUENCE, 11 unordered pieces.

AC023276
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                                                                                                                         1.195. 1.12.4

Anote—14 copies 20 mer 87% conserved"
27196. 27267

Anote—18 copies 4 mer tctc 93% conserved"
2765. 27268

Anote—18 copies 4 mer tctc 93% conserved"
2765. 31089

Anote—2 copies 20 mer 100% conserved"
3029. 31630

Anote—2 copies 20 mer 100% conserved".
31206. 33289

Anote—12 repeat: matches 3. 37 of consensus"
34316. 34870

Anote—12 repeat: matches 1619. 2094 of consensus"
34816. 33289

Anote—12 repeat: matches 1619. 2094 of consensus"
34816. 33289

Anote—12 repeat: matches 16. 3.00 of consensus"
34816. 33289

Anote—12 repeat: matches 1. 301 of consensus"
34816. 35203

Anote—14 repeat: matches 1. 301 of consensus"
35204. 35204

Anote—14 repeat: matches 5620. 5894 of consensus"
35204. 35205

Anote—14 repeat: matches 5620. 5894 of consensus"
35209. 35575

Anote—14 repeat: matches 10. 312 of consensus"
36208. 36209

Anote—14 repeat: matches 10. 312 of consensus"
36208. 36309

Anote—14 repeat: matches 2006. 2346 of consensus"
36208. 36609. 36609

Anote—14 repeat: matches 2006. 2346 of consensus"
36208. 36609. 36609. 38609. 38609. 38609. 38609. 38725

Anote—14 repeat: matches 2006. 2346 of consensus"
36208. 36609. 38609. 38725

Anote—25 repeat: matches 2006. 2346 of consensus"
36208. 36609. 38609. 38725

Anote—26 copies 2 mer tt 73% conserved"
36608. 38609. 38609. 38725

Anote—36 copies 2 mer ttaa 86% conserved"
36608. 38609. 38725

Anote—36 copies 2 mer ttaa 86% conserved"
36608. 38725
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copies 4 mer acac 100% conserved"
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/note="24 copies 2 mer aa 72% conserved"
complement(42583. .43000)
/note="match: GSS: Em:AQ753378"
/note="MER5A repeat: matches 41. .96 of 6
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                                   /note="2 copies 38 mer 93% 27195. .27274
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AL591127
Mus musculus chromosome 2 clone RP23-370H21, *** SEQUENCING IN PROGRESS ***, in unordered pieces.
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Sims, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-JUN-2001) Sancer Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Jun 8, 2001 this sequence version replaced gi:14329610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 163357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1016 others
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HTG; HTGS_PHASE1; HTGS_FULLTOP.
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                                                                                                                                                               10437. 14644
/note="assembly_name:Contig35"
/note="assembly_name:Contig36"
18503. 30764
/note="assembly_name:Contig36"
                                                                                                                                                                                                                                                                                                                                       30865. ...45533
/note="assembly_name:Contig38"
45634. ...67543
/note="assembly_name:Contig39"
67644. ...93006
/note="assembly_name:Contig40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93107. .122817. //note="assembly_name:Contig41" | 122918. .163357 //note="assembly_name:Contig42" | 30271 c 30821 g 50170 t
                                                                 /note="assembly_name:Contig33"
                        /note="assembly_name:Contig32"
3082. .6638
                                                                                       6739. .10336
/note="assembly_name:Contig34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 atcacttgaccctactctacctgggctggactgggtg 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
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30865. .45533
                                                                                                                                             vector_side:right"
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75.7%;
                                                                                                                                   clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 56.5
Best Local Similarity 75.7
Matches 28; Conservative
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Submitted (10-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On May 28, 2000 this sequence version replaced gi:7887466.
                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 163357)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * uns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; 93%
Sequencing vector: M13; 93%
Sequencing vector: plasmid; 7%
Chemistry: Dye-primer ET; 93% of reads
Chemistry: Dye-primer ET; 93% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 157652 bases at least 040
Consensus quality: 158635 bases at least 030
Consensus quality: 158636 bases at least 030
Insert size: 171000; agarose-fp
Insert size: 171000; agarose-fp
Insert size: 162357; sum-of-contigs
Quality coverage: 5.57 in 020 bases; sum-of-contigs
Quality coverage: 5.95 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                          Center: Washington University Genome Sequencing Center
Center code: WUGSC
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gap of unknown length
contig of 3557 bp in length
gap of unknown length
contig of 3598 bp in length
gap of unknown length
contig of 4208 bp in length
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67543: contig of 21910 bp in length
67643: gap of unknown length
93006: contig of 25363 bp in length
93106: gap of unknown length
122817: contig of 29711 bp in length
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contig of 3658 bp in length
gap of unknown length
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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  AC023276.4 GI:8099962
HTG; HTGS_PHASE1; HTGS_DRAFT.
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Waterston, R.H.
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14744:
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                                                                 Homo sapiens
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6639
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Gaps

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HSG1150 178660 bp DNA linear PRI 22-OCT-1999
Homo sapiens chromosome 21 PAC LLNLP704G1150Q13, complete sequence.
AJ006996
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Insert size: 170972; 5.1% error; agarose-fp
Quality coverage: 8.92x in Q20 bases; sum-of-contigs Quality
                                                         * NOTE: This is a 'working draft' sequence. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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21846. .26926
/note="assembly_fragment:03415
fragment_chain:1"
27027. .38936
/note="assembly_fragment:04311
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                  96647. .14334

/note-"assembly_fragment:03790

fragment_chain:1"

114435. .146124

/note-"assembly_fragment:04597

fragment_chain:1"

148225. .172385

/note-"assembly_fragment:00491

fragment_chain:1"
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Pred. No. 35;
0; Mismatches 9;
                             coverage: 9.01x in 020 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                          38997. .96546
/note="assembly_fragment:00142
fragment_chain:1"
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fragment_chain:1
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                                                                                                                                                /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="2"
/clone="RP23-370H21"
                                                                                                                                                                                                         /clone_lib="RPCI-23"
1. .21745
                                                                                                                     Location/Qualifiers
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Best Local Similarity
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AUTHORS
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HSG1150
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Prior probability: 0.04; Overlapping number: 0 > Xpound (Thomas
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Database(s): * RepBase (human), released 22-DEC-1995.
* RepBase (primate), released 22-DEC-1995.
Minimum identity: 70 %,
> 'ESTS': BLASTN 2.0.9 (Altschul et al.)
Database(s): * embl (EST), vers. 60 (16-SEP-1999)

* emblnew (EST), Vers. 60+ (12-OCT-1999). Using unmasked
                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum score: 60; Minimum identity: 70 %;

> 'Tandem Repeats': GDE 2.2 option 'tandem'
Minimum length 2 bp: Maximum length 20 bp: Score threshold 20
Treat N's as mismatches? YES: Allow uniform consensi? NO >
'Inverted Repeats': GDE 2.2 option 'inverted'
> 'Micro Satellites': GDE 2.2 option 'sputnik' (Abajian) > 'CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CpG island region size 100 bp;
Minimum GC contents 50 %; Observed/Expected 0.6 > 'STS Scan';
PCR (Schuler)
Margin: 50; Number of mismatches allowed: 0; Word size: 7.
STS database: 'dbSTS markers'
> 'tRNA Scan': tRNAscan-SE (Lowe & Eddy), Vers. 1.11.
Location/Qualifiers
1. 178660
/Organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1."
/clone="LLNLP704G1150013"
                                                                                    Max Planck Institute for Molecular Genetics
Intestrasse 73, D-14195 Berlin-Dahlem, Germany
Sequence overlaps with Acc. Mr. AJO06995
All annotations in this database entry are developed by
computational tools. It is therefore not explicitly noted in the
feature lines that evidence is not experimental.
PROGRAMS AND PARAMETERS USED FOR ANNOTATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Using unmasked
                                                                                                                                                                                                                                                                                                                        Analysis and annotation were performed with the automatic first-pass' annotation and submission tool 'AnnoMitter' (Hornischer & Bloecker).
Programs used by 'AnnoMitter':
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complement(1. .30)

/note="xPOUND prediction, score = 0.393"

complement(166. .507)

/note="83% identity: matches 4. .345 of consensus"

/rpt_family="THE1b"
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/note="match: ESTs AA74429 AA745355 AA745582"
complement(779. 835)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum score: 60; Minimum identity: 70 %; > 'GSSs': BLASTN 2.0.9 (Altschul et al.) Database(s): * embl (GSS), Vers. 60 (16-SEP-1999) * emblnew (GSS), Vers. 60+ (12-OCT-1999) . Using
GBF, Dept. of Genome Analysis
Mascheroder Weg 1, D-38124 Braunschweig, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Organism: Humman
SenScan (Burge & Karlin), Vers. 1.0
Grail (Xu et al.), Vers. 1.3
Organism: human
Macef (Zhang)
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/note="match:_ESTs_AA744088_AA744074"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      > GeneFinder (Green), Vers. 084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Organism: human
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/rote="9598 identity: matches 410. .515 of consensus"
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2 (Dases I to 340000)

Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T., Park,H.S., Toyoda,A., Ishli,K., Totoki,Y., Chol,D.K., Soeda,E., Ohki,M., Takagi,T., Sakaki,Y., Taudlen,S., Blechschmidt,K., Polley,A., Menzel,U., Delaber,J., Kumpf,K., Lehmann,R., Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A., Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K., Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S.,
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                                                                                                                                      .393 of consensus"
                                                         of consensus"
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8273. .8364
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/note="CpG_island (%GC=59.8, o/e=1.07, #CpGs=15)"
complement(8268. .3364)
/note="97% identity: matches 132. .228 of consensu
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Homo sapiens genomic DNA, chromosome 21q, section 44/105.
AP001700 AL163245 BA000005
AP001700.1 GI:7768710
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Best Local Similarity 75.7%; Pred. No. 35;
Matches 28; Conservative 0; Mismatches
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AUTHORS
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// cote="homology = 79.1%, counts = 13"
// Tpt_family="atatacacacac repeat"
// Tpt_type=TANDEM
2506. .2600
// cote="AC repeat"
2530. .2582
// note="IR1, 79% complementary to IR1' (3707. .3759)"
// Tpt_type=INVERTED
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complement(3435. .3561)

/note="84% identity: matches 134. .260 of consensus"

/rpt_family="AluJb"

3440. .3537

/note="Genefinder prediction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6683. .6695

/note="TC repeat"

complement((7117.7208). .7546)

/note="match: GSS B14745 B59625"

complement(7586. .7640)

/note="MAEF prediction, score = 0.568"

/791. .7803

/note="TC repeat"

complement(8072. .8088)
                                                                            complement(2020. .2135)
/note="XPOUND prediction, score = 0.379"
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/note="homology = 95.8%, counts = 12"
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/rpt_type=TANDEM
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1984. .2091
/note="Genefinder prediction"
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/note="TTTA repeat"
8178. .8225
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/rpt_family="LINE/LI"
/rpt_type=DISPERSED
6798. 6847
/note="LilMA4A"
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/rpt_type=DISPERSED
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/note="(CAA)n"
/rpt_family="Simple_repeat"
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8282. 8343
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                                                                                                                                                                                                                                   /rpt_family="SINE/Alu"
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complement(6954. .7127)
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/rpt_family="LinE/Li"
/rpt_family="LinE/Li"
/rpt_family="LinE/Li"
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/rpt_family
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/rpt_type=DISPERSED
complement(4100, .4253)
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                                                                                                              /rpt_family="LINE/LI"
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2535. .2818
/note="Aluy"
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11589. .11659
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11661, .11847
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2209. .2521
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Antonarakis, S.E., Minoshima, S., Shimizu, N., Nordsiek, G., Hornischer, K., Barandt, P., Scharfe, M., Schoen, O., Desario, A., Reichelt, J., Kauer, G., Bloceker, H., Ramser, J., Beck, A., Klages, S., Hennig, S., Riesselmann, L., Dagand, E., Wehrmaeyer, S., Borzym, K., Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and
                                                                                                                                                                                           Direct Submission
Submitted (10-APR-2000) to the DDBJ/EMBL/GenBank databases. The
Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic
Sciences Center, Human Genome Research Group * Institute of
Molecular Biotechnology, Genome Analysis * Kelo University School
of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome
Analysis * Max-Planck Institute for Molecular Genetics (addresses
                                                                                                                                                                                                                                                                                                                                                                                                                    see below)
On May 30, 2000 this sequence version replaced gi:7717301.
The chromosome 21 mapping and sequencing consortium consisting of
* RIKEN Genomic Sciences Center, Human Genome Research Group, *
Sagamihara 228-8555, Japan,
* e.mall: hattori@gsc.riken.go.jp
* URL: http://hgp.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kelo University School of Medicine, Molecular Biology, * Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * GBF, Dept. of Genome Analysis,
* Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
Info.genome@gbf.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * Institute of Molecular Biotechnology, Genome Analysis, Beutenbergstrasse 11, D-07745 Jena, Germany, * e.mail: gscj-submit@genome.imb-jena.de * URL: http://genome.imb-jena.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * Max-Planck Institute for Molecular Genetics,
* Innestrasse 73, D-14195 Berlin, Germany,
* e.mail: info-chr21@molgen.mpg.de
* URL: http://chr21.rz-berlin.mpg.de/
**AL163245: Submitted (10-Apr-2000).
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* e.mail: nshimizu@dmb-med.keio.ac.jp
* URL: http://www.dmb.med.keio.ac.jp/
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/note="(TG)n"
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pH: 8.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
Dermatology, Box 8123, 660 South Euclid Avenue, St. Louis, MO 63110, USA
Tel: 314-362-8162
Fax: 314-362-8159
Email: hamideh@psts.wustl.edu
Primer A: TGACATGATAGCACCAAGCAC
Primer B: GGAAAGCTGTCAGGATCCAG
STS size: 333
PCR Profile:
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Denaturation: 93 degrees C for 10 seconds
Annealing: 60 degrees C for 1.00 minute
Polymerization: 72 degrees C for 1.00 minute
PCR cycles: 35
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13911. 14148
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16873. 17238
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Pul-Yan Kwok
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   repeat_region
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AUTHORS
TITLE
JOURNAL
COMMENT
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G42160

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                                                                                                                                                                                                                                                                                                                                                          56.0%; Score 22.4; DB 11;
81.2%; Pred. No. 40;
tive 0; Mismatches 6;
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1. .33
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                                                                                                                                                                                                                                                                                  complement(312. .333)
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Job time: 6733 sec
                                                                                                                                                                       Location/Qualifiers
1. .333
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Best Local Similarity 81.23
Matches 26; Conservative
                                                                                                        MGC12: 1.5 mM
KC1: 50 mM
Tris-HC1: 10 mM
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0 19 23 57.5 0 20 23 27.5 0 24 23 57.5 0 24 23 57.5 0 25 23 27.5 0 25 23 57.5 0 27 23 57	
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1 ctcgagccaccccataaccctcaatactccagggattggg 40 13736207 seqs, 6748477542 residues IDENTITY_NUC Gapoxt 1.0 US-09-721-543A-13 Title: Perfect score: Scoring table: Sequence: Searched:

27472414 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

em_estba:*
em_esthum:*
em_estin:*
em_estin:*
em_estov:*
em_estpl:*
em_estpl:* EST: * Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

AW845395 CM4-CT004
BF740572 QV1-HB003
T08487 EST06378 In
T92497 Ye24b09.r1
BE878784 601493062
AW804230 PM3-UM008
BE005490 CM1-BN011
BF005492 CM1-BN011
BF005492 CM1-BN011
BF094424 RC1-WT003
BF089733 QV0-BT070
BF540702 GC2055458
BF09734 GC2055458
BF005486 CM1-BN011
AA327421 EST30756
BF07773 GC205268
BF07773 GC2052818
BG1057734 GO1462081 Description SUMMARIES AW845395 TOB487 T92497 T92497 BEC96490 BEC05490 BEC05492 N73434 BEC05492 N73434 BEC05492 BEC05492 BEC05486 AA327421 BEC05201 AW804233 010000000 Query Match Length DB 661.8 Score Result No. ပ $\circ \circ \circ$ Ü ပပ 0000

BE622136 601440862 BG288188 602383704 BE89496 601445061 BE894967 601443612 AA101534 Zn79C11.s AA383010 EST96488 BE878754 601493017 BF848202 QVO-EN005 BE61777 601441968 BC390247 60234494 T39447 ya06a08.r1 BF778852 PM1-H7060 AA384401 EST97914 AA53875 MTBCae09 AW804241 PM3-UM008 T39458 ya06b07.r2 AW804241 PM3-UM008 AA38479 EST96599 BE936437 RC1-NT003 BE936437 RC1-NT003 BF968657 602214628 BF968657 602214628 BF968657 602214628 BF968657 602214628 BF115712 PM0-ET020	BF884828 PMO-ET020 AA361993 EST71440
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ALIGNMENTS

RESULT 1

AW845395/C DEFINITION ACCESSION VERSION VERSION VERSIO	AW845395 CW4-CT0045-180200-512-a09 CT0045 Homo sapiens CDNA, mRNA sequence. AW845395 AW845395. GI:7940912 EST. Houman. Houman. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. J (bases 1 to 296) Dias Neto.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Boldan,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., da Silva,W.J. Soares,F., Warstein,A., da Silva,W.J. Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J. Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J. Shotgun sequencing of the human transcriptome with ORF expressed proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663 Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Faz: +55-11-270492
FEATURES	High quality sequence stop: 200. Location/Qualifiers
77 1700	/230 /organism="Homo sapiens"

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Gaps

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us-09-721-543a-13.rst

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250 bp mRNA linear EST 03-AUG-1993 EST06578 Infant Brain, Bento Soares Homo sapiens CDNA clone HIBBE96 5, end, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 250)
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84 c 72 g 31 t 7 othe
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932 Clopper Road, Gaithersburg, MD 20878
Tel: 3018699056
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76.9%; Pred. No. 35;
ive 0; Mismatches
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Seq primer: M13 Reverse.
Location/Qualifiers
            6
            110
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T08487.1 GI:389515
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T92497.1 GI:724410
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nes 28; Conservative
          129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 3018699423
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          BASE COUNT
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 486) Dias Ito 480. Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J.
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Email: asimpson@ludwig.org.br
This asquence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=QVi&t2-QVI-HB0031-
071200-561-e06&t3=2000-12-07&t4=1)
Seq primer: puc l8 forward
High quality sequence start: 8
High quality sequence start: 8
Liocation/Qualifiers
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
                                                                                                                                                                                                                                                                                   Score 24.6; DB 9; Length 296;
Pred. No. 31;
0; Mismatches 9; Indels
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/db_xref="taxon:9606"
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BF740572.1 GI:12067248
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76.9%;
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Fax: +55-11-2707001
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1 (bases 1 to 69)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                                                                     Insert Size: -97
Insert Size: 37
Insert Size: 331
High quality sequence stops: 324
Source: IMAGE Consortium, LLNL
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RPl
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                                                                                                                                 Contact: Wilson RK
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 337;
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/db_xref="taxon:9606"
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/clone_lib="Stratagene lung (#937210)"
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1 Similarity 74.4%; Pred. No. 76;
29; Conservative 0; Mismatches 10;
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Location/Qualifiers
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AWBU4230 110300-002-d06 UM0089 Homo sapiens CDNA, mRNA sequence. AWB04230
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM3-UM0089-170
300-002-d0&&t3=2000-03-17&t4=1)
Seq primer: puc lB forward
High quality sequence start: 23
High quality sequence stop: 118.
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                                                                                                                                                                                              /clone_lib="NIH_MGC_69"
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/tab_host="lub (phage-resistant)"
/note="Organ: lung: Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
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Sukaryota; Metazoa; Chordatu; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 118)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
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/db_xref="taxon:9606"
/clone_lib="UM0089'
/dev_stage="Adult"
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                                                                                                                                             /organism="Homo sapie
/db_xref="taxon:9606
http://image.llnl.gov
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High quality sequence stop: 6
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Best Local Similarity 74.4%;
Matches 29; Conservative
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Best Local Similarity 74.4 Matches 29; Conservative
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CMI-BN0117-110 seq primer. puc 18 forward
High quality sequence start: 18
High quality sequence stop: 135.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 135)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
from ORESTES PCR (U.S. Letters Patent application No. 196. 776 - Ludwig Institute for Cancer Research) profiles into the DVC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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20202663
                                                                                                                                                                                           Score 23; DB 9; Length 118; Pred. No. 98;
                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                      68 TCCACCCACACTTGAAGCCACAAAACTGCAGGGATTGGG 30
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37 g 29 t
                                                                                     stringency conditions."
31 c 35 q 2
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                                                                                                                                                                                           57.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                   29; Conservative
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BE005490
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Length 135;

DB 9;

Score 23;

Query Match

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 147)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nogai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., W.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-CM1-BN0117-110
400-183-hod&t3-2000-04-11&t4-1)
Seq primer: puc 18 forward
High quality sequence stop: 147.
                                                                                                                                                                                                                                                                                    BE005492 110400-183-h04 BN0117 Homo sapiens cDna, mRNa sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                   Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Pred. No. 1e+02;
0; Mismatches 10; Indels
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Pred. No. 1e+02;
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43 c 39 g 31 t
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/clone_lib="BN0117"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                  BE005492
BE005492.1 GI:8265725
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Best Local Similarity 74.4%;
Matches 29; Conservative
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N73434/c
LOCUS
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ACCESSION

VERSION KEYWORDS

SOURCE

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Tel: +55-11-2704922
Fax: +55-11-270001
Fax: +55-11-270001
This solution and defived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/sr.ripts/sqethtm12.pl?tl=&t2=RC1-NT0033-110 Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="NT0033'
/dev_stage="Adult"
/note="Organ: nervous_tumor; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derlived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludvig Institute for Cancer Research)
profiles into the pUC 18 vector: Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 208)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvahlo, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE089733 22: bp mRNA linear EST 12-JUN-2000 QVO-BE0704-120500-224-c08 BT0704 Homo sapiens cDNA, mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 223)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Balia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bubher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Pred. No. 1.1e+02;
0; Mismatches 10
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62 c 51 g 42 t
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
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Best Local Similarity 74.43
Matches 29; Conservative
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AUTHORS
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     KEYWORDS
SOURCE
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                                                                                                                                                                                                                                          manufactor burneria; Filmates; Catallini; Hounillage; Holmo.

S. Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, W., DuBuque, T., Favello, A., Gish, W., Hawkins
, M., Hultman, M., Kucaba, T., Lecy, M., Le, M., Le, N., Mardis, E., Moore
, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thlerry-Meg, J., Trevaskis, E.,
Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
Genome Res. 6 (9), 807-828 (1996)

E. Genome Res. 6 (9), 807-828 (1996)

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Fax: 314, 286 1810
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/tissum...type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_nost="bH10B (amplcillin resistant)"
/note="Vector: pT713D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
: 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF090424 2000 208 bp mRNA linear EST 19-OCT-2000 RCI-WT0033-110900-111-C09 NT0033 HOMO sapiens CDNA, mRNA sequence. BF090424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Revin G. Becker (NINDS/NIH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1021 Std Error: 0.00
Seq primer: reverse ET
High quality sequence stop: 145.
Location/Qualifiers
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TGTTACCAATCIGAAGIGGGAGCGGCCGCAITTITITITITITITIT 3'),
31e12.rl Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA one IMAGE:284686 5', mRNA sequence.
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/db_xref="GDB:3903214"
/db_xref="taxon:9606"
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/clone=lib="Soares_multiple_sclerosis_2NDHMSP"
/sex="male"
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                  Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QVO-BT0704-120
500-224-co86x13-200-05-12&t4=1)
500-224-co86x13-200-05-12&t4=1)
Figh quality sequence start: 12
High quality sequence stop: 223.

Location/Qualifiers
1. .223
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 225)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                      Shotgun sequencing of the human transcriptome with ORF expressed
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM9499 row, d column: 16
High quality sequence stop: 225.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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74.4%; Pred. No. 1.1e+02;
ive 0; Mismatches 10;
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/db_xref="taxon:9606"
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/dev_stage="Adult"
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BF340702
BF340702.1 GI:11287151
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Matches 29; Conservative
Simpson, A.J.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/dlone="IMAGE:4183263"
/clone="IMAGE:4183263"
/clone_type="glioblastona with EGFR amplification"
/tissue_type="glioblastona with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned uniditectionally. Primer: Oligo dT. Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Fax: +55-11-2707001
Fax: +55-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtm12.pl?tl=&t2=CM1-BN0117-110 Seq primer: puc 18 forward 400-183-e05453=2000-04-11644=1)
High quality sequence start: 17
High quality sequence start: 17
High quality sequence story: 227.
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//Organism="Homo sapiens"
//Organism="Homo sapiens"
//Obxerel="taxon:9606"
//Clone_lib="Bw0117"
//dev_stage="Adult"
//note="Organ: breast_normal; Vector: pucl8; Site_l: SmaI; Site_2: SmaI; A minl-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
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Bukazyota; Merazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Bukazyota; Merazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 227)
Dias Neto.E., Garcial Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J.
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Laborationary of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                               AA327421 231 bp mRNA linear EST 20-APR-1997 EST30756 Colon I Homo sapiens CDNA 5' end similar to similar to TEGT, mRNA sequence.
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For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
tissue mRNA and cDNA amplification were performed under low stringency conditions." 69\ c 54\ g 50\ t
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EcoR1; Site_2: XhoI"
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                                                                                                                                                          Length 227;
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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                                                                                                                                                     Query Match 57.5%; Score 23; DB 9; 18est Local Similarity 74.4%; Pred. No. 1.2e+02; Matches 29; Conservative 0; Mismatches 10
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COMMENT
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BF037734 237 bp mRNA linear EST 20-OCT-2000
601462081F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865269 5',
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/db_xref="taxon:6606"
/clone=lib=NHL MGC_66"
/clone=lib=NHL MGC_66"
/tissue_type="adenocarcinoma"
/tissue_type="adenocarcinoma"
/hab_host="hHl0B (phage-resistant)"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Salı; Cloned unidirectionally. Primer: Oligo dr.
/note=ginsert size 1.8 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manala; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 237)
NIH-MGC http://mgc.ncl.nih.gov/.
NIH-MGC http://mgc.ncl.nih.gov/.
Wational Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAW9608 row: b column: 22
High quality sequence stop: 237.
Location/Qualifiers
1. 237
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57.5%; Score 23; DB 9; 11 11 12 14.4%; Pred. No. 1.2e+02; Conservative 0; Mismatches 10
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Job time: 4528 sec
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Matches 29; Conservative
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BF037734
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us-09-721-543a-13.rni

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June 4, 2002, 17:47:09; Search time 116.71 Seconds (without alignments) 84.186 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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SUMMARIES	ID	US-08-818-514-1	US-08-818-514-2	US-09-115-934A-1	US-09-115-934A-2	US-08-735-609-9	US-08-735-609-9	US-09-315-372-9	US-09-244-752-9	US-09-245-497-9	US-09-221-235-10	US-09-221-928-10	US-09-221-527-10	US-09-221-236-10	US-09-221-416-10	US-09-221-245-10	US-09-163-115-10	US-09-221-528-10	US-09-593-553-10	US-09-221-237-10	US-08-770-379-20	US-08-757-669A-20	US-09-230-371A-20	US-08-742-009-2	US-09-172-110-2	US-08-317-880-3	-08-782-39	US-09-364-230-5
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1132 - 4 - 4 - 4 - 4 - 4 - 4 - 4 - 4 - 4 -	ALIGNMENTS tor Protei tor Protei bos 1.0, Versi 8,5:4 5:46	re 23; DB cd. No. 0.8 Mismatches ccagggattg
US-08-132-990A-3 US-08-317-880-1 US-08-317-880-1 US-08-493-197-3 US-08-493-197-3 US-08-493-197-3 US-09-120-601-3 US-09-120-601-3 US-09-120-601-3 US-09-120-601-3 US-09-120-601-3 US-09-120-601-3 US-09-120-601-3 US-09-120-601-3 US-08-477-630-10 US-08-477-630-10 US-08-477-630-10 US-08-477-630-10 US-08-477-630-10 US-08-472-293-10	ALIGNMENTS BB18514 Inhibitor Proteins Flores Village Drive, Suit tible SOS/MS-DOS tease #1.0, Version S/O8/818,5:4 M. A. 11,815 TION: 11,815 FITTON: 11,8	Score Pred. // Mis actcca
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	Application 1837838 S837838 S837838 IF. Reed, John IF. Reed, John IF. Xu, Qunl1 IF. Xu, Qunl1 IF. SEQUENCES: WDENCE ADDRES. SED Diego California IF. United St. 4370 La Jo. San Diego California IF. United St. 4370 La Jo. San Diego Ganpbell E FORE TYPE: Flopp ER: IBM PC C. TYPE: Flopp ER: IBM PC C. TYPE: Plopp TYPE: PL	lty serva cata
4444444444444444 000000000000000000000	Application Applic	Cons cons accc
44440000000000000000	ULT 1 08-818-514-1/c equence 1, Application us atent No. 5837838 GENERAL INFORMATION: APPLICANT: Reed, John APPLICANT: Xu, Quull TITLE OF INVENTION: B NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSEE: CAREET: 4370 La JOI. CITY: San biego STREET: 4370 La JOI. CITY: San biego STREET: Galifornia COUNTRY: United States INFORMATION EN STATE: COMPUTER: ENDADLE FORM MEDIUM TYPE: Floppy COMPUTER: BM PC CON OPERATING SYSTEM: CORPUTER: IBM PC CON OPERATING SYSTEM: CONFRYING SYSTEM: FLING DATE: FLING DATE: FLING DATE: FLING DATE: FLEFAX: (619) 535- TELEFAX: (619) 5	Simi 9; agcc ACCC
	J.T. 1 Juence 1, Appuence 2, A	Query Match Best Local Matches 2 2 tcg 11 2056 TCC
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57.5%; Score 23; DB 3; Length 2634; 74.4%; Pred. No. 0.81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Reed, John C.
APPLICANT: Xu, Qunli
TITLE OF INVENTION: BAX Inhibitor Proteins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,934A
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                                                                   FILING DATE: 14 MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 3209
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 3209
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/818,514
FILING DATE: 14-WAR-1997
ATTORNEY/AGENT INFORMATION:
                                                     US 08/818,514
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ZIP: 92122
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2: SEGUENCE CHARACTERISTICS:
LENGTH: 2634 base pairs
                                                                                                                                                                                                                                                                                                  LENGTH: 2634 base pairs
TYPE: nucleic acid
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STATE: California
COUNTRY: United States
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Best Local Similarity 74.4
Matches 29; Conservative
                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Pred. No. 0.81;
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APPLICANT: Xu, Qunla
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STREE California
COUNTRY: United States
                                                                                                                                                                                                   ADDRESSEE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                COMPUTER REAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,514
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,934A
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                  Sequence 2, Application US/08818514
Patent No. 5837838
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Xu, Qunli
TITLE OF INVENTION: BAX Inhibitor Proteins
UNMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-901
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.58;
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 74.4*
Matches 29; Conservative
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Gaps

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Kumar-Singh, Ralendra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-315-372-9/c
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                                                     Gaps
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              DB 3; Length 2634; 0.81;
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                                                     Indels
                                                                                                                                                                                                                                                                                 APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Hauser, Michael A.
APPLICANT: Harigan-O'Connor, Dennis J.
ITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,609
                                                 10;
                                                                                                              579 TCCACCCACACTTGAAGCCACAAAACTGCAGGGATTGGG 617
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                                                                                          2 tcgagccaccccataaccctcaatactccagggattggg
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              Score 23; DB
Pred. No. 0.81
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Ingolla, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOOKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States Of America ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESCRIPTION: /desc - "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amalfitano, Andrea
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                                                                                                                                                                                                                             Sequence 9, Application US/08735609
Patent No. 5955360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
            Query Match 57.5%;
Best Local Similarity 74.4%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3364 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
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Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Matches
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                                                                                                                                                                                                                                            COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OE/735,609
FILING DATE: 23-OCT-1996
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09315372
Patent No. 6057158
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Manaerian, Michael A.
APPLICANT: Harser, Michael A.
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES:
CORRESPONDENCE ANDRESS:
Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
                                                                                          ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 20; DB 2
Pred. No. 15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-841C
FELFERAT: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    STATE: California
COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     United States Of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 72.2%;
Matches 26; Conservative C
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                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                        Query Match 50.0%; Score 20; DB 3; Length 3364; Best Local Similarity 72.2%; Pred. No. 15; Matches 26; Conservative 0; Mismatches 10; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/245,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Haursingh, Rajendra
APPLICANT: Hartigen-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                            2326 AGCCTGCCCTCACCCTGGATCCACCAGGGACAGGG 2291
                                                                                                                                                                                                                                                                                                    5 agccacccataaccctcaatactccagggattggg 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 agccacccataaccctcaatactccaggattggg 40
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APPLICATION NUMBER: 08/735,609
APPLICATION NUMBER: 08) FILING DATE:
ATTORNEY/FAGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-838
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3364 base pairs
TYPE: nucleic acid
STRNDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-09-245-497-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States Of America ZIP: 94104
                       TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
SESCRIPTION: /desc = "DNA"
US-09-244-752-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/09245497
Patent No. 6083750
GENERAL INFORMATION:
    3364 base pairs
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Best Local Similarity 72.2
Matches 26; Conservative
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-245-497-9/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Hauser, Michael A.
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2326 AGCCTGCCCCTCACCCTGGATCCACCAGGGACAGG 2291
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NAME: Ingolia, Diane E.
REGISTRATHON NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: US/09/315,372
                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/735,609
FILING DATE:
                                                                                                                                                                                                      UM-02484
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                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "DNA"

US-09-315-372-9
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APPLICATION NUMBER: 08/735,609
FILING DATE:
                                                                                                                                                    NAME: Ingglia, Diane E.
REGISTRATION NUMBER: 40,027
REFRENCE/DOCKET NUMBER: UM-07
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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Patent No. 6063622
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TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          LENGTH: 3364 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-244-752-9/c
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STATE:
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APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-050
CURRENT APPLICATION NUMBER: US/09/22:,527
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,135
EARLIER FILING DATE:
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 1864
TWO DELINED THE NOVEL TO THE NOVE
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APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-050
CURRENT APPLICATION NUMBER: US/09/221,236
CURRENT FILING DATE: 1998-12-28
EARLIER FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTI VET. 2.0
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APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-050
CURRENT APPLICATION NUMBER: US/09/221,416
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
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Best Local Similarity 67.5%; Pred. No. 29;
Matches 27; Conservative 0; Mismatches 13;
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48.0%; Score 19.2; DB 3;
Best Local Similarity 67.5%; Pred. No. 29;
Matches 27; Conservative 0; Mismatches 13;
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Patent No. 6153417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (275)..(754)
US-09-221-527-10
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ORGANISM: Homo sapiens
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; LOCATION: (275)..(754)
US-09-221-236-10
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US-09-221-236-10
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LENGTH: 1864
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Patent No. 6121030

GENERAL INFORMATION:
APPLICANT: Acton, Susan
TILLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR FILE REFERENCE: MNI-050
CURRENT FILLING DATE: 1998-12-28
CURRENT PILLING DATE: 1998-12-28
EARLIER FILLING DATE: NUMBER: 09/163,115
EARLIER FILLING DATE: NUMBER: 097163,115
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 1864
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Pred. No. 29;
0; Mismatches
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67.5%; Pred. No. 29
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; Patent No. 6043040
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Best Local Similarity 67.5%;
Matches 27; Conservative
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Best Local Similarity 67.5
Matches 27; Conservative
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US-09-221-928-10
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US-09-221-235-10
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LENGTH: 1864
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US-09-221-928-10
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TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: MIN-050
CURRENT APPLICATION NUMBER: US/09/221,245
CURRENT APPLICATION NUMBER: US 09/163,115
EARLIER APPLICATION NUMBER: US 09/163,115
EARLIER APPLING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
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48.0%; Score 19.2; DB 4; Length 1864;
Best Local Similarity 67.5%; Pred. No. 29;
Matches 27; Conservative 0; Mismatches 13; Indels 0
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48.0%; Score 19.2; DB 3; Length 1
Best Local Similarity 67.5%; Pred. No. 29;
Matches 27; Conservative 0; Mismatches 13; Indels
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Job time: 6584 sec
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US-09-221.245-10
'Sequence 10, Application US/09221245
'Patent No. 6180358
'GENERAL INFORMATION:
BARLIER FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 1864
TYPE: DNA:
TYPE: DNA:
PRATURE:
FRATURE:
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; LOCATION: (275)..(754)
US-09-221-416-10
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ORGANISM: Homo sapiens
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; LOCATION: (275)..(754)
US-09-221-245-10
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LENGTH: 1864
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Ligand; human cytomegalovirus; HCMV infection; herpetic ulcer; pneumonia; gastroenteritis; chorio:etinitis; antiviral agent; herpesvirus infection; lesion; ds.
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AAS85386
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AAX37525
ABL06092
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AAS91288
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ABA20005
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AAI91505
AAS43104
AAA43173
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AAI37184
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ABL32625
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AAK91137
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Human foetal liver
Probe #16250 for g
Human brain expres
                                                                     June 4, 2002, 17:56:12; Search time 521.5 Seconds (without alignments) 131.690 Million cell updates/sec
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Bax inhibitor BI-1
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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| SIDSI/gcgdata/geneseqn-embl/NA1981.DAT:*
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                         1736436 seqs, 858457221 residues
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Maximum Match 100%
Listing first 45 summaries
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AAV59067
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Human immune/haema
DNA encoding novel
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Human foetal liver

Probe #5870 used t

Human secreted

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Human brain expres

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Polynucleotide ligands useful as arti-viral agents for the treatment of

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Liu F, Wang J, Jiang

WPI; 2001-367658/38.

Human bone marrow Probe #20651 used Human foetal liver

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Human immune/haema

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Probe #7579 used t

bone marrow

Probe #6388 for ge Human brain expres

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herpesvirus infections e.g. primary or chronic infections with human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW73136), of the pro-apoptotic protein Bax. Nucleic acids encoding BI-1 and BI-2 (see AAV59068) were identified by suppression of Bax-induced death of yeast cells transformed to express human Bax. A human HepG2 cDNA library was used for library screening. The invention provides vectors, optionally expression or viral vectors, containing BI nucleic acids, and host cells containing these vectors. The nucleic acids encoding BI-1/BI-2 can be used to
                                                                                         herpesvirus, particularly human cytomegalovirus (HCMV) to decrease or block HCMV infection in target cells. These ligands are used as anti-viral agents for the treatment of herpesvirus infections (e.g. lesions and herpetic ulcers) and particularly HCMV associated
                                                                                                                                                  primary or chronic infections such as pneumonia, gastroenteritis and chorioretinitis. The present sequence is DNA ligand which bind to HCMV to decrease or block HCMV infection in target cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bax inhibitor proteins, BI-1 and BI-2 - useful e.g. to modulate cellular apoptotic activity or identify agents altering BI-1 or binding which can modulate apoptotic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA clone codes for an inhibitor protein, termed BI-1 (see
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                                                                          The invention relates to polynucleotide ligands which bind to
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Pred. No. 1.1e-07;
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                                         8; Page 6; 60pp; English.
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                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bax inhibitor BI-1 cDNA
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                 cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 xu o;
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                                            Claim
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Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; and antagonists may have neuroprotective; cytostatic; cardioactive; and antagonists may have neuroprotective; cytostatic; cardioactive; gastrointestinal general; nephrotropic; antilnfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences. The lung cancer associated polynucleotide sequences. The protein of lung cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat associates such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18433 and
                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; prollferative disorder; wound healing; infectious disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer -
                                                                                                                                                                                                                                   Gaps
increase expression of these proteins in cells, or antisense molecules prepared from them used to decrease expression. In these ways, cellular apoptotic activity may be modulated (claimed). The nucleic acids and complementary sequences are also useful as probes to detect BI-encoding nucleic acid molecules in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; lung cancer assoclated protein; neuroprotective; cytostatic;
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                                                                                                                                                                                           DB 19; Length 2634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer associated polynucleotide sequence SEQ ID 73.
                                                                                                                                                                                                                                 Indels
                                                                                                                            Sequence 2634 BP; 632 A; 626 C; 597 G; 779 T; 0 other;
                                                                                                                                                                                                                                                                                           2056 TCCACCCACACTTGAAGCCACAAAACTGCAGGGATTGGG 2018
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                                                                                                                                                                                       Score 23; DB 19
Pred. No. 4.1;
0; Mismatches
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                                                                                                                                                                                         57.58;
74.48;
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                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 29; Conserv
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Probe #16250 for gene expression analysis in human heart cell sample.
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234587.
                                                                                  ABA37784 standard; DNA; 121
                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00666
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                                                                                                                                          (first entry)
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                                              ABA37784;
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                                                                     ABA37784/C
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                                                                                                                                                                                                                                                                                                                                                                   Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Wote: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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                                                                                                Length 2922;
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                                                                                                                                                                                                                                                                                                                                       Human foetal liver single exon nucleic acid probe #19974.
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                                                       Sequence 2922 BP; 712 A; 686 C; 654 G; 863 T; 7 other;
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                                                                                                                          10;
                                                                                              21;
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                                                                                              Score 23; DB 2
Pred. No. 4.2;
0; Mismatches
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                                                                                                                                                                                                                                                       BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0207456.
2000US-0608408.
2000US-0632366.
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1 Similarity 74.4%;
29; Conservative
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ID ABA71669 standard; DNA; 121
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                                                                                                                                                                                                                                                                                                           (first entry)
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Best Local Similarity 76.5'
Matches 26; Conservative
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                                                                                                             Local Similarity
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30-JUN-2000;
03-AUG-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single exon nucleic acid probes for analyzing gene expression in human hearts -
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Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertens.on; cardiac arrhythmia; congenital heart disease; ss.
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0; Mismatches
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ID AAK200
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
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                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
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2000US-0207456.
2000US-0608408.
2000US-023466.
2000US-0234687.
2000US-0234587.
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27-SEP-2000; 2000US-0236359
04-OCT-2000; 2000GB-0024263
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WO200157276-A2
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30-JUN-2000;
03-AUG-2000;
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
21 - SEP - 2000;
04 - OCT - 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple scierosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                               Human; brain expressed exon; gene expression analysis; probe; microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; SEQ ID NO: 20004; 650pp + Sequence Listing; English.
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                                                                               Human brain expressed single exon probe SEQ ID NO: 20004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21.2; |
Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                   26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0508408.
03-MOZ-2000; 2000US-0633366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
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ilarity 76.5%;
Conservative
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                                             05-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                  epilepsy; cancer; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-483446/52
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Best Local Similarity
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                                                                                                                                                                                                                   WO200157275-A2
                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                   04-FEB-2000;
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              AAK20013;
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AAK46055/c

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Length 121; Indels

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Sequence 473 BP; 144 A; 91 C; 95 G; 143 T; 0 other;
 probe of the
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03-AUG-2000;
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27-SEP-2000;
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26-MAY-2000;
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                                                                                                                                                       The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
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                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human foetal liver single exon nucleic acid probe #7450.
                                                                                                                                                                                                                                               Sequence 121 BP; 46 A; 20 C; 28 G; 27 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                    7 ccaccccataaccctcaatactccagggattggg 40
                                                                                                                              Claim 25; SEQ ID No 20651; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                 DR;
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(MOLE-) MOLECULAR DYNAMICS INC
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                              Chen W,
                                                                                                                                                                                                                                                                                        ch 53.0%;
1 Similarity 76.5%;
26; Conservative
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-053366.
21-SEP-2000; 2000US-0234687.
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                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-483447/52
                                                      WPI; 2001-488897/53
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                            Penn SG,
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Matches
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe #6388 for gene expression analysis in human heart cell sample.
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                                                                                                                                                                                                                      Length 473;
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                                                                                                                                                                                                                                                                                  Indels
                                                                                                                        BP; 144 A; 91 C; 95 G; 143 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                        347 CCTTCCTATAATCCTCATACTCAAGGTAATGGG 314
                                                                                                                                                                                                                                                                                                                                        40
                                                                                                                                                                                                                   Score 21.2;
Pred. No. 18;
                                                                                                                                                                                                                                                                            0; Mismatches
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2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                Query Match 53.0%;
Best Local Similarity 76.5%;
Matches 26; Conservative
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ID ABA27922 standard; DNA; 473
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2000US-0236359
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                                                                                                                           Sequence 473
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Matches

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe #7579 used to measure gene expression in human placenta sample.
                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for
                                                                                                  Human bone marrow expressed single exon probe SEQ ID NO: 7652.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analyzing gene expression in human bone marrow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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AAK33095 standard; DNA; 473 BP.
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2000US-0207456.
2000US-0608408.
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30-JUN-2000; 2000US-0608408
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234697.
27-SEP-2000; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the probes of the invention.
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                                                                    (first entry)
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Matches 26; Conservative
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                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in human brains {\color{black} \cdot}
                                                Gaps
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              Length 473;
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                                                                                                                                                                                                                                                                                                         Human brain expressed single exon probe SEQ ID NO: 7321.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
              DB 22;
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                                                                                                  347 CCTTCCTATAATCCTCATACTCAAGGTAATGGG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40
                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 ccaccccataaccctcaatactccagggattggg 40
            Score 21.2;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21.2;
                                                                              7 ccaccccataaccctcaatactccagggattggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.0%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000; 2000US-0608408.
03-MG-2000; 2000US-052366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0235596.
04-OCT-2000; 2000GB-0024263.
          53.0%;
76.5%;
                                                                                                                                                                                                   AAK07330 standard; DNA; 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                                                                     05-NOV-2001 (first entry)
                                            26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                               epilepsy; cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-483446/52
        Query Match
Best Local Similarity
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es 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Penn SG,

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Gaps

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Length 473; Indels

22; ..

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WO200157272-A2.

Query Match

Best Loc Matches

ò q RESULT 12 AAK33095/c

us-09-721-543a-13.rng

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Duan DR,
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Best Local Similarity
Matches 28; Conserv
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                                        02-OCT-1997;
02-OCT-1997;
                    02-0CT-1997;
02-0CT-1997;
02-0CT-1997
02-0CT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; diagnosis; cancer; tummour; neurodegenerative disorder; developmental abnormality; fetal deficiency; blood disorder; leukemia; immune system disease; autoimmune disease; hepatic disease; lymphoma; renal disease; inflammation; allergy; Alzheimer's disease; schizophrenia; cognitive disorder; prostate disease; skelatai, cardiac; muscle disorder; pulmonary disorder; transplant rejection; osteoclast; osteoporosis; arthritis; malignancy; digestive; endocrine; infection; ss.
                                                                                                                                                                                                                                                     The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secreted protein; treatment; prevention; protein therapy; AIDS;
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                 ch 53.0%; Score 21.2; DB 22; Length 473; 1 Similarity 76.5%; Pred. No. 18; 26; Conservative 0; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein cDNA fragment containing gene 75.
                                                                                                                                                                                                                                                                                                                   Sequence 473 BP; 144 A; 91 C; 95 G; 143 T; 0 other;
                                                                                                                                                                                                              analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                       347 CCTTCCTATAATCCTCATACTCCAGGTAATGGG 314
                                                                                                                                                                                                                                                                                                                                                                                            7 ccaccccataaccctcaatactccagggattggg 40
                                                                                                                                                                                                                                Claim 25; SEQ ID No 7579; 654pp; English.
                                                                                                                                                          Rank DR;
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                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                          Chen W,
                                                                                2000US-0632366.
2000US-0234687.
2000US-0236359.
2000GB-0024263.
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97US-0060836.
97US-0060837.
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                              30-JAN-2001; 2001WO-US00663
                                                              2000US-0207456.
2000US-0608408.
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                                                  2000US-0180312
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                                                                                03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                   04 - FEB - 2000;
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02-OCT-1997;
02-OCT-1997;
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proteins they encode. The products of the invention are useful for preventing, treating or ameliorating medical conditions, e.g. by protein preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by cetermining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 101 polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and fetal deficiencies, blood disorders, developmental abnormalities and fetal deficiencies, blood disorders, lawkemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, Alzheimer, sand cognitive disorders, pulmonary disorders, transplant rejection, disorders involving osteoclasts such as costeoporosis, arthritis or malignancies, disease, schizophrene disorders, infections and ADDS. The human secreted proteins of the invention are corrected by the content of the content of the corrected are content of the content of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human genes and the secreted polypeptides they encode
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      uan DR, Endress GA, Feng P, Ferrie AM;
Greene JM, Janat F, Lafleur DW, Ni J;
ben SM, Shi Y, Young P, Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 837 BP; 171 A; 249 C; 187 G; 228 T; 2 other;
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Pred. No. 29;
0; Mismatches 12;
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97US-0060838.
97US-0060839.
97US-0060843.
97US-0060862.
97US-0060866.
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70.0%;
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Florence KA, Giec.
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Search completed: June 4, 2002, 17:56:14 Job time: 7102 sec

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Homo sapiens CDNA: FLJ22952 fis, clone KAT09742.

AK026605.1 GI:10439494

Oligo capping; fis (full insert sequence).

Homo sapiens signet ring cell carcinoma cell_line:KAT0 III cDNA to Homo sapiens.
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AC087620 Homo sapi
AC016997 Homo sapi
AC020991 Homo sapi
AL093645 Homo sapi
AL035631 Human DNA
AL13483 Homo sapi
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35 Homo sapi
47 Homo sapi
67 Homo sapi
67 Homo sapi
83 human DNA
99 Trypanoso
53 Human DNA
11 Homo sapi
14 Homo sapi
89 Trypanoso
11 Homo sapi
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Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H.,
Ota,T., Sızuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
Nakamura,Y., Isogai,T. and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sugano, S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AC009611
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                                                                                                                                                            NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5' - 6 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5 3' - 5
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Submitted (14-JAN-1994) L. Walter, Abteilung Immungenetik der
Submitted (14-JAN-1994) L. Walter, Abteilung Immungenetik der
Universitaet Goettingen, Gosslerstr 12d, 37073 Goettingen, FRG
2 (bases 1 to 2600)
Walter.L., Marynen,P., Szpirer,J., Levan,G. and Gunther,E.
Identification of a novel conserved human gene, TEGT
Genomics 28 (2), 301-304 (1995)
Sugano, Institute of Medical Science, University of Tokyo,
Laboratory of Genome Structure Analysis, Human Genome Center;
Shirokane-dal, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdnaii, a-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
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/clone="KATO9742"
/note="KRTO742"
/note="cloning vector pME185FL3"
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/tissue_type="testis"
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/organism="Homo sapiens"
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X75861.1 GI:456258
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NVFFGSIWLFQANLXVGLVVMCGFVLFDTQLIIEKABHGDQDXIWHCIDLFLDFITVF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2609)
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Submitted (16-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                               Gaps
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Homo sapiens, testis enhanced gene transcript, clone MGC:5230
IMAGE:2900280, mRNA, complete cds.
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., G
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu,
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MGC help desk family capabs-remain. 1900 famil: capabs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing Center Sequencing Center College of Medicine Human Genome Sequencing Center
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                                                                                                                                                                  Length 2600
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/tissue_type="Placenta, chorlocarcinoma"
/clone_lib="NHL_MGC_10"
/lab_nost="0H108"
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Pred. No.
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/db_xref="taxon:9606"
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BC000916.1 GI:13111818
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74.48;
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Matches 29; Conservative
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Homo sapiens chromosome 12 clone RP11-161E16, WORKING DRAFT SEQUENCE, 24 unordered pieces.
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                                     PAT 16-MAY-2001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Unclassified.
I (bases 1 to 2634)
S Reed J.C. and Xu.Q.
Bax inhibitor proteins
Location/Qualifiers
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1.2634
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Pred. No. 31;
0; Mismatches
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1 (bases 1 to 2634)

Reed,J.C. and Xu.Q.

Bax inhibitor proteins

Patent: US 6130317-A 2 10-02T-2000;

Location/Qualifiers
                                2634 bp
Sequence 1 from patent US 6130317.
AR112791.1 GI:14092691
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Sequence 2 from patent US 6130317,
AR112792
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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597 c 626 g
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74.48;
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Best Local Similarity 74.4%;
Matches 29; Conservative
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Reed, J.C. and Xu.O.
Bax inhibitor proteins
Patent: US 5837838-A 2 17-NOV-1998;
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Bax inhibitor proteins
Patent: US 5837838-A 1 17-NOV-1998;
Location/Qualifiers
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Sequence 2 from patent US 5837838.
AR058921 GI:5984498
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Sequence 1 from patent US 5837838.
AR058920
                                                          Score 23;
Pred. No. 3
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1 625 c 602 g
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597 c 626 g
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nilarity 74.4%;
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                of 15466 bp in length
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/note="assembly_name:Cont1g13"
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/note="assembly_name:Contig14"
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18692. :58168
note="assembly_name:Contigl7"
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11075. .48591
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/note="assembly_name:Contig18"
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/note="assembly_name:Contigl9"
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55625, .173416
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173517. .197189
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Anote-"assembly_name:Contig7"

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Anote-"assembly_name:Contig8"
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121943. .137362
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'note="assembly_name:Contig4"
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/note="assembly_name:Contig5"
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note="assembly_name:Contig6"
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/note="assembly_name:Contig9"
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/note="assembly_name:Cont1921
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
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gap of
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108055. .121842
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                                                                        Direct Submission
Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Mar 13, 2000 this sequence version replaced gi:7021812.
                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                         Center: Washington University Genome Sequencing Center
Center code: WUGSC
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              Waterston, R.H.
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Query Match
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1 (bases 1 to 21586)

1 (bases 1 to 21586)

2 Mazny, D. M., Adams, C., Adio-Oddola, B., Ali-Osman, F.R., Balks, T., Barbaria, Barks, T., Barbaria, Benten, J., Barton, E., Barvan, B., Baryar, T., Barbaria, J., Bentcon, J., Enterew, Barbaria, Baryar, Barbaria, Bentcon, J., Blange, K., Blankenburg, K., Bonnin, D., Garron, T.F., Carter, M., Cavazos, S.R.; Chackon, J., Chavez, D., Cox, C., Chowdhry, I., Christopolos, C., Chen, G., Chen, R., Chen, C., Chowdhry, I., Christopolos, C., Chen, G., Chen, G., Chen, C., Chowdhry, I., Christopolos, C., Chen, G., Chen, C., Denn, A.L., Dugar, C., Dutbin, K., Deladao, C., Edaren, E., Edaren, C., Harriade, C., Harris, K., Harriade, C., Harris, E., Howard, S., Hamer, J., Jak, Y., Johnson, E., Jolloway, C., Hollins, B., Jackson, E., Kally, S., Khan, U., King, L., Kovah, J., Kovar, C., La, J., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, R., Marling, E., Martin, R., Marling, E., Marten, E., Maher, S., Marthin, R., Marten, C., Miner, C., Shen, P., Pace, A., Pavton, S., Gorder, C., Shen, M., Rojas, A., Rojas, A., Poylbokan, L., Rolfe, M., Rojas, M., Rojas, A., Tabor, P., Taneria, R., Taneria, R., Sodergren, E., Sonaker, T., Sparks, A., Solasy, R., Salaton, A., Stalto
                                                                                                                                                                                                                                                                                     HTG 31-JAN-2002
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Submitted (11-07-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                     Gaps
                                                                                                                                                                                                                                                                               ACO84037 215867 bp DNA linear HTG 31-,
Homo sapiens chromosome 12q clone RP11-382G3, WORKING DRAFT
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On Jan 31, 2002 this sequence version replaced gi:15809132.
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0
DB 2; Length 197189;
                       Pred. No. 27;
0; Mismatches 10; Indels
                                                                                                                                  AC084037.28 GI:18449688
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                  2 togagocaccccataaccctcaatactccagggattggg 40
Score 23;
                                                                                                                                                                                                                                                                                                                                     SEQUENCE, 7 unordered pieces.
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57.5%;
                       Best Local Similarity 74.4
Matches 29; Conservative
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AC084037
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ACC90998 225818 bp DNA linear HTG 31-JAN-2002 Homo sapiens chromosome 12q clone RP11-161816, WORKING DRAFT SECONDENCE, 20 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                         Consensus quality: 223543 bases at least Q40
Consensus quality: 227846 bases at least Q30
Consensus quality: 229698 bases at least Q20
Estimated insert size: 217093; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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Pred. No. 27;
0; Mismatches 10; Indels 0;
                                                                                                                                                                                                                                      Chemistry: Dye-primer Bodipy: 2% of reads
Chemistry: Dye-terminator Big Dye: 98% of reads
Assembly program: Phrap; version 0.990329First of
findPhrapList
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of 12534 bp in length gap of unknown length contig of 12920 bp in length gap of unknown length length contig of 6274 bp in length gap of unknown length
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gap of unknown length
contig of 80431 bp in length
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of 80431 bp in length
unknown length
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Center: Baylor College of Medicine
Center code: BCM
                                                                                                                                                                      Sequencing vector: Plasmid; M77789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="RP11-382G3"
51141 c 50650 g 54279 t
                                                                  Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                         Sequencing vector: M13; L08821
                                                                                                                                                 Center clone name: RP11-382G3
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                                                                                                                        Center project name: HCHJ
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74.4%;
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1 (Dasca I to Albaba)

Subarburoks, S. L., Amaratunge, H.C., Arej. R., Altosman, F.R., Allen, C., Alsbrooks, S. L., Amaratunge, H.C., Arej. R., Ayele, M., Banks, T., Barbarden, J., Benton, J., Blankehurg, K., Bondin, D., Bouck, J., Bowle, S., Birkehurg, R., Bondin, D., Bouck, J., Bowle, S., Birkehurg, R., Brown, B., Brown, M., Bryant, N.P., Bubay, C., Burch, F., Burkett, C., Burrell, R., Brown, R., Bryant, N.P., Carton, T.F., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, R., Chen, R., Chen, R., Chen, R., Chacko, J., Chavez, D., Chen, R., Chen, R., David, R., David, R., David, C.D., Cox, C., Coyle, M.D., Dathorne, S. R., David, R., David, L., Davis, C., Dany, Carroll, L., Ding, Y., Dinh, H.H., Douthwalte, K. J., Draper, H., Dugan-Rocha, S., Unbin, K., J., Earnhart, C., Edgar, D., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferragulo, D., Farmer T. Garza, N., Gill, R., Goo, J., Garcia, A., Garner T. T., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner T. Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner T., Garza, N., Gill, R., Gabisi, A., Howard, C., Harris, K., Harr, M., Havlak, P., Hawes, A., Harnandez, O., Harris, K., Harr, M., Havlak, P., Hawes, A., Harnandez, J., Harnandez, O., Jia, Y., Johnson, R., Johlvet, S., Joudan, S., Warlboson, B., Jia, Y., Johnson, R., Johlvet, S., Joudan, S., Markins, J., Lu, X., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulesged, H., Massey, E., Mawhiney, E., Martin, R., Martinger, M., Marting, R., Marting, E., Massey, E., Mawhiney, E., Matchell, T., Mobabbat, R., Morgen, M., Moyen, N., Nguyen, N., Nguyen, N., Nickerson, E., Micchell, T., Mobabbat, R., Morgen, R., Morgen, R., Morgen, R., Morgen, R., Morgen, R., Morgen, R., Pull, L., Oulles, M., Ren, Y., Stone, H., Shooshtari, N., Nguyen, N., Nickerson, E., Nwoken, W., Stone, H., Shooshtari, N., Nguyen, N., Nguyen, N., Nickerson, E., Nwoken, W., Stone, H., Shooshtari, N., Nguyen, N., Wall, M., Wall, K., Wall, M., Wall, K., Wall, M., Wall, K., Wall, M., Wall, M., Y., Wall, Y., Wa
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On Jan 31, 2002 this sequence version replaced gi:15625966.
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Assembly program: Phrap; version 0.990329First call to
findPhrapList
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Weinstock,G. and Glbbs,R.
Direct Submission
                                                                                (bases 1 to 225818)
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Direct Submission
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TITLE

COMMENT

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Homo sapiens chromosome 18 clone RP11-873L22 map 18q21, WORKING DRAFT SEQUENCE, 18 unordered pieces.
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
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                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
            NOTE: This sequence may represent more than one clone. NOTE: This is a "working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is
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g of 51451 bp in length
f unknown length
g of 20945 bp in length
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95645. .109592

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129356. .13700

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                                                                              04: gap of 100 bp 67070: contig of 19966 bp in length 70: gap of 100 bp 1057: contig of 15587 bp in length
                                  23: gap of 100 bp
47004: contig of 21981 bp in length
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150760 .155896
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82858. .95544
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/note="assembly_fragment"
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/db_xref="taxon:9606"
          contig of
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                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (29-MAY 2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, 10RL:http://ngp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
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                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 171185)
Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fuliyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 171,185 genomic DNa of 18621
Published Only in Database (2000) In press
(bases 1 to 171185)
Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: PCR products; 100% of reads Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of Assembly program: Phrap; version 0.990329 Consensus quality: 156977 bases at least Q40 Consensus quality: 164110 bases at least Q30 Consensus quality: 167421 bases at least Q20 Insert size: 169485; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: RIKEN Genomic Sciences Center (GSC)
Center code: RIKEN
Web Site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
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                                                    HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:RP11-873L22.
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center clone name: RP11-873L22
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Length Length length

BASE COUNT

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Sequence updated (26-May-2000).

* NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will.

* be preserved.
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23793 23892; gap of 100 bp
23893 45465; contig of 21573 bp in length
45466 45565; gap of 100 bp
45566 58167; contig of 12602 bp in length
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142674 146286; contig of 3613 bp in length
146287 146386; gap of 100 bp
146387 150053; contig of 3667 bp in length
150054 150153; gap of 100 bp
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Homo sapiens chromosome 18 clone RP11-859C21 map 18q21, WORKING AP001569

AP001569

AP001569

AP001569: GI:8117403

HTG: HTGS_PHASE1: HTGS_DRAFT.

Homo sapiens DNA: clone:RP11-859C21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (29-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-855, Japan (E-mail:hattoriegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, On May 30, 2000 this sequence version replaced gi:7380904.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Pujlyama,A., Yada, T., Tokoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission.
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167805. .169750
/note="assembly_fragment"
169851. .171185.
/note="assembly_fragment"
a 32086 c 33289 g 52078 t
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Best Local Similarity 79.4%;
Matches 27; Conservative
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

AUTHORS JOURNAL REFERENCE TITLE

DEFINITION ACCESSION

LOCUS

RESULT 1 AP001569

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in length in length

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23792 contig of 45465 contig of

23893

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Birren, B., Lincon, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 18, clone hRPK.411_H_24

Homo sapiens chromosome 18, clone hRPK.411_H_24

Homo sapiens chromosome 18, clone hRPK.411_H_24

To bases 1 to 179726)

Birren, B. Lincon, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barter, J., Baldwin, J., Barna, N., Beckerly, R., Denria, D., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, R., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Tones, C., Jones, C., Kann, L., Raratas, A., Lebocky, J., Liau, C., Locke, K., Macdonald, P., Marduis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Mala, M., Mortis, W., McKernan, K., McLaughlin, J., Mala, M., Mortis, W., McKernan, K., McLaughlin, J., Nalloff, M., O'Connor, T., O'Connell, P., Pavilin, B., Peterson, K., Pollara, V., Riley, R., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassiliav, H., Vo, A., Wagner, A., Waylor, J., Wyman, D., Ye, W.J. and Zody, M. Direct Submission Submitted (09-MAR-1999) Whitehead Institute/MIT Center for Genome Research, 20 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 17925)

Birren, B. Linton, L., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Devar, K., McKernan, K., McKernan, K., McMan, D., Gardyna, S., Gilbert, D., Garata, M., Mortis, M., McDiff, M., O'Connor, T., O'Connor, N., Depayre, E., Devon, K., McKernan, K., McKernan, R., McKernan, K., McKernan, K., McKernan, K., McKernan, K., McKernan, K., McKernan, K., McHerson, M., McDwan, P., McGurk, A., McKernan, K., McHerson, M., Mortis, M., Mortis, M., McDwan, P., McGurk, A., McKernan, R., Weder, M., Severy, P., Stange-Thomann, W., Stojanovic, N., Stone, C., Jones, C., Jones,
                                                                                                                                                                                                                                                                                                                                                                                                 AC007052 179726 bp DNA linear PRI 23-MAR-1999
Homo sapiens chromosome 18, clone hRPK.411_H_24, complete sequence.
AC007052
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Direct Submission
Submitted (23-MAR-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 24, 1999 this sequence version replaced 91:4432872.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179726)
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                                                                                                                                    Indels
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                                                                                                      Pred. No. 33;
   /note="assembly_fragment"
                                                                     Score 22.8;
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                                                                  57.0%;
                                                                                                                                    Conservative
                                 Query Match
Best Local Similarity
Thes 27; Conserve
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Query Match 57.0%; Score 22.8; DB 9; Length 179726; Best Local Similarity 79.4%; Pred. No. 33; Matches 27; Conservative 0; Mismatches 7; Indels 0; /rpt_famlly="AluJo" 36366) 36525. 36587 7rpt_famlly="ArIch" 36792. 36840 /rpt_family="BC200" complement(4347. .24514) /rpt_family="MER21B" 24782. .2500 /rpt_family="AT_rich" complement(27113. .27422) /rpt_family="AluSp" 27865. .28190 /rpt_family="MIR"
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Gaps

KEYWORDS VERSION

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soon as it is available and the accession number will
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69099 103010: contig of 33912 bp in length
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                                                                        804 903: gap of 100 bp 904 1787: contig of 884 bp in length 1788 1887: gap of 100 bp 100 bp 3003: contig of 1116 bp in length 1888 103: gap of 100 bp 100 bp
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of 1989 bp in length
                                                                                                                                                                                                                                                                                                 7588 7687: gap of 100 bp
7688 9739: contig of 2052 bp in length
9740 9839: gap of 100 bp
9840 13254: contig of 3415 bp in length
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13355 17739: contig of 4385 bp in length
                                                          contig of 803 bp in length
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1. .803
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Pred. No. 33;
0; Mismatches
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/organism="Homo sapiens"
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gap of
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/map="18"
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACO90408 182411 bp DNA linear HTG 09-MAY-2001 Homo sapiens chromosome 18 clone RP11-859C21 map 18, WORKING DRAFT SEQUENCE, 14 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 182411)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 6.2 in Q20 bases; sum-of-contigs
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Sequencing vector: Plasmid: n/s 100% of reads
Sequencing vector: Plasmid: n/s 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 177348 bases at least Q40
Consensus quality: 179869 bases at least Q30
Consensus quality: 180657 bases at least Q30
Insert size: 181111; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence_submissions@genome.wi.mit.edu------- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 18, clone RP11-859C21 Unpublished
                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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Web site: http://www-seq.wi.mit.edu
Db 78718 CTCTAGCCTCCCATGCCCCTCATTCTCCCAGTG 78685
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AC090408.2 GI:13357356
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AC090408/c
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Gaps

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/note="L1PB3 repeat: matches 5916. .6147 of consensus"
                                   3969. .4006
/note="U2 re
4392. .4430
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This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, annotated human repeat sequence elements (e.g. Alu), where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                          188357 bp DNA linear PRI 24-JUL-2000 Human DNA sequence from clone RP11-401F12 on chromosome 9. Contains ALI59996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Bm:, SMSSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9

RR11-401F12 is from the library RPCI-11.2 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 188357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is the entire insert of clone RPII-401F12 The true left end of clone RPII-208G24 is at 167549 in this sequence. The true right end of clone RPII-395D3 is at 5200 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (19-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clonerequest@sanger.ac.uk
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/note="2 copies 32 mer 96% conserved"
2698. .2698
duplicated flanking sequence represents the duplicated flanking sequence of the TN10."
3529. .3560
/note="8 copies 4 mer gtgt 96% conserved"
3746. .3959
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/note="LIMC4 repeat: matches 6462. .7077 of
410. .897
/note="match: GSS: Em:AQ606829"
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/note="match: GSS: Em:AQ823967"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="RPCI-11.2"
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8. .1231 of consensus"
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/note="match: GSS: Em:AQ787911"
27777. .28867
/note="ilMC3 repeat: matches 6667. .7734 of consensus"
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/note="L2 repeat: matches 2357. .2612 of consensus" 15947. .16013
10013. .12 repeat: matches 2609. .2674 of consensus" 16084. .16364
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                                                                                                                                                                                                                                                                                                                                                                                                              /note="19 copies 2 mer tg 92% conserved" 12615. 12650 /note="6 copies 6 mer gtgtgt 91% conserved" 13805. 14099 /note="Alusy repeat: matches 2. .295 of conserved" 14101. 14388
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         1392. .4430
/note="13 copies 3 mer aac 92% conserved"
 of
                                                                                                                                                                                                                                                                      11880. 12174
/note="L2 repeat: matches 1...
complement(12504. 12890)
/note="match: STS: Em:HSA311YC1"
/note="match: STS: Em:HSA311YC1"
/note="match: STS: Em:HSA311YC1"
.38
                                                                                                                                                                                                                                                                                                                                                                             /note="10 copies 4 mer gtgt 90%
12610. .12647
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complement(1624, 16783)
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Job time: 6659 sec

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7; Indels

Search completed: June 4, 2002, 17:46:31

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June 4, 2002, 15:53:27; Search time 4272.65 Seconds (without alignments) 126.357 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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RESULT 1 AW845395/c	LOCUS	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM		REFERENCE	AUTHORS	ě				TITLE		JOURNAL	MEDLINE	COMMENT													SEAMINGS	SOUTCE		

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4 gagccaccccataaccctcaatactccagggattgg 39
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Location/Qualifiers
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Matches 30; Conservative
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Site_l: SmaI; A mini-library was made by cloning products
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No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 486)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Email: asimpson@ludwig.org.br
This asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=QV1&t2=QV1-HB0031-
071200-561-e06&t3=2000-12-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence start: 8
Location/Qualifiers
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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20202663
                                                                                                                                                                                                                                           Length 296;
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ye24b09.rl Stratagene lung (#937210) Homo sapiens cDNA clone
IMAGE:118649 5', mRNA sequence.
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1 (bassa 1 to 250)
Adams, H.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J.C. Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library Nature Genet. 4, 373-380 (1993)
Contact: Adams, MD
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DB 10;
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932 Clopper Road, Gaithersburg, MD 20878
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/db_xref="taxon:9606"
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Matches 29; Conserv
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1 (bases 1 to 69)

1 (bases 1 to 69)

2 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

3 National Institutes of Health, Mammalian Gene Collection (MGC)

3 Contact: Robert Strausberg, Ph.D.

4 Contact: Robert Strausberg, Ph.D.

5 Email: cgapbs-remail.nih.gov

7 Tissue Procurement: DCTD/DTP/Gazdar

5 CDNA Library Preparation: Life Technologies, Inc.

5 CDNA Library Preparation: Life Technologies, Inc.

5 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

5 DNA Sequencing by: Incyte Genomics.

5 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_atgge="72 years"
//dev_atgge="72 years"

,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Mortis,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Prange,C., Rifkin,L., Rohlfing,T., Challenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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Insert Size: 331
High quality sequence stops: 324
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="GDB:486938"
/db_xref="taxon:9606"
/clone="IMAGE:118649"
/clone_lib="Stratagene lung (#937210)"
/sex="male"
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L Similarity 74.4%; Pred. No. 76;
29; Conservative 0; Mismatches 10;
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Location/Qualifiers
1. .337
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Fax: 314 286 1810
Email: est@watson.wustl.edu
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Homo sapiens
Bukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Merata; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 118)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW804230 110300-002-d06 UM0089 Homo sapiens cDNA, mRNA sequence.
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                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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/tissue_type="largs cell carcinoma, undifferentiated"
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/note="Organ: lung: Vector: pCMV-SPORT6; Site_1: Not1:
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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86;
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/db_xref="taxon:9606"
/clone_lib="UM0089"
/dev_stage="Adult"
http://image.llnl.gov
plate: LLAM968 row: k colu
High quality sequence stop: 6
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Conservative
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us-09-721-543a-12.rst

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Best Local Similarity 74.4 Matches 29; Conservative
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM1-BN0117-110 Seq primer: puc 18 forward
1400-183-908&t3=2000-04-11&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 135.
Location/Qualifiers
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref
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1 (bases I to 135)

1 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J.
from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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СМ1-BN0117-110400-183-908 BN0117 Homo sapiens CDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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20202663
                                                                                                                                                                                                                                                                                                         DB 9; Length 118;
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40 c 37 g 29 t
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Pred. No. 9
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                                                                                                                                                                                                                                                                                                         57.58;
74.48;
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Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Length 135;

Score 23; DB 9;

57.5%;

Query Match

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Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpsoneludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-CM1-BN0117-110 400-183-hodgsi3-200-04-118t4=1)

Seq primer: puc 18 forward: High quality sequence stop: 147.
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dclone_lib="BN0317"
/dev_stage="Adult"
/note="Organ: breast_normal; Vector: puc18; Site_1: Smal;
Site_2: Smal; A min1-library was made by cloning products
Gerived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector: Reverse transcription of
tissue manA and cDNA amplification were performed under
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 147)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Sliva,W. Jr., Zago,M.A., Bordin,S., Coste,F.F.,
Magal,M.A., da Cliva,W. Jr., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
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                                                                                                                                                                                                                                                                                    BE005492 110400-183-h04 BN0117 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
                                                   Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 1e+02;
0; Mismatches 10; Indels
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Pred. No. 1e+02;
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43 c 39 g 31 t
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BE005492.1 GI:8265725
                     74.48;
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Best Local Similarity 74.4%;
Matches 29; Conservative (
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S Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins
, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, M., Mardis, E., Moore
, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan', F., Thierry-Wag, J., Trevaskis, E.,
Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
Genome Res. 6 (9), 807-828 (1996)
E 9704478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314, 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pr7730 (Pharmacia) with a modified polylinker V_TYPE: phagemid; Site_1: Not I: Site_2: Eco RI : 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  double stranded cDNA was size selected, ligated to Eco'RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTyT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH). 3 t
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                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1021 Std Error: 0.00
Seq primer: reverse ET
High quality sequence stop: 145.
Location/Qualifiers
yz31e12.rl Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNAclone IMAGE:284686 5', mRNA sequence.
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/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
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                                               N73434.1 GI:1230719
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                                             ACCESSION
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KEYWORDS
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/db_xref="taxon:9666"
/db_xref="taxon:9666"
/clone_lib="Nr0033'
/dev_stage="Adult"
/note="Organ: nervous_tumor; Vector: pucl8; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
3 a 62 c 51 g 42 t
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Fax: +55-11-2707001

Bmail: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl~&t2-RC1-NT0033-110
900-111-c098513-2000-09-118ti=1)
Seq primer: puc 18 forward
High quality sequence stop: 208.

Location/Qualifiers
Homo sapiens
Bukaryota, Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 208)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W.Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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Eukaryota; Metazoa; Chordatu; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin!; Hominidae; Homo.

1 (bases 1 to 223)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bodial,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F.; Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunsteain,A., deoliveirae, P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
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20202663
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BE089733.1 GI:8480168
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Location/Qualifiers
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Best Local Similarity 74.4
Matches 29; Conservative
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AUTHORS
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/organism="Homo sapiens"
/do.xef="texon:9606"
/clone_lib="BT0704"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: breast; Vector: pucl8; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bassa 1 to 225)

1 (bassa 1 to 225)

2 NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CLONG distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Floud Albayog row: d column: 16

High quality sequence stop: 225.
                                                                                                                                                                                                                             Fax: +55-11-270701
Email: asImpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QVO-BT0704-120
500-224-c08&t3=2000-05-12&t4=1)
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                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
             Shotgun sequencing of the human transcriptome with ORF expressed
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                                               Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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74.4%; Pred. No. 1.1e+02;
tive 0; Mismatches 10
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High quality sequence start: 12
High quality sequence stop: 223.
Location/Qualifiers
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Fax: #52-11-2./10/001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM1-BN0117-110 400-182-e09&t3-2000-04-11&t4-1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence store: 227.
Location/Qualifiers
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Location/Qualifiers
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Above="Romo sapiens"
Above="Romo sapiens"
Above="Romo sapiens"
Acloe="Lib="BN0117"
Ade_stage="Adult"
Anin1-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No 196,716 - Ludwig Institute for Cancer Research)
Profiles into the PUC 18 vector. Reverse transcription of
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammala; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 227)
Dlas Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Naqai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Fax: +55-11-2707001
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Gaps

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Length 231;

Score 23; DB 9; I Pred. No. 1.2e+02; 0; Mismatches 10;

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57.5%;
ilarity 74.4%;
Conservative (
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    Query Match
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 231)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

3. (J., Lee, M.H., Kirkness, E.F., Weinstock, K.G., Gocapho, J.D., White

3. (J., Lee, M.H., Kirkness, E.F., Weinstock, K.G., Cacapho, J.D., White

3. (J., Lee, M.H., Kirkness, E.F., Meinstock, K.G., Cacapho, J.D., White

3. (J., Lee, M.H., Kirkness, E.F., Meinstock, K.G., Capton, R.A.,

3. (J., Lee, M.H., Kirkness, E.H., Handon, R.C., Man-Wai, C., Clayton, R.A.,

3. (J., Liu, D., Earle-Hughes, J., Fine, L.D., Fitzgerald

3. (J., Liu, L.I., Marmaros, S.M., Merrick, J.M.,

4. (Kelley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M.,

5. (Spring, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

7. (Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

8. (Musch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L.,

8. (M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and
                                                                                                                                                                                                                                                                                                                                                  AA327421 20-APR-1997 EST30756 Colon I Homo sapiens CDNA 5' end similar to similar to TEGT, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
tissue mRNA and cDNA amplification were performed under low stringency conditions." 69\ c 54\ g 50\ t
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/note="Organ: colon; Vector: pBluescript SK-; Site_1:
EcoR; Site_2: XhoI"
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                                                                                                                                                                  10; Indels
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Pred. No. 1.2e+02;
0; Mismatches 10;
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/db_xref="taxon:9606"
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Location/Qualifiers
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                                                                                                                        Query Match 57.5%;
Best Local Similarity 74.4%;
Matches 29; Conservative
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KEYWORDS
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                                            BASE COUNT
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ORIGIN
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AUTHORS
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BF037734 237 bp mRNA linear EST 20-OCT-2000 601462081F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865269 5',
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SITE (Dases 1 to 237)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs.remail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Sanomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://magge.llnl.gov

Plate: LLAM9608 row: b column: 22

High quality sequence stop: 237.
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/db_xref="taxon:9606"
/clone="InMdE:3865269"
/clone=lib="NHL WGC_66"
/tissue_type="adenocarcinoma"
/lab_host="PHIOB (phage-resistant)"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Salı; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
                                                                                                                                                                                                     Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Job time: 4527 sec
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48 c 62 g
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Best Local Similarity 74.4
Matches 29; Conservative
                                                    mRNA sequence.
BF037734
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STATE: California
COUNTRY: United for the country of the country o
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS:
SOFTWARE: PatentIn Release #1.6, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,514
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US-08-782-396-1
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PCT-US95-07844-3
US-09-102-072-3
US-09-122-071-23
US-09-102-011-224-1
US-09-071-224-1
US-09-071-224-3
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Pred. No. 0.81;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, John C.
APPLICANT: Xu, Qunli
TITLE OF INVENTION: BAX Inhibitor Proteins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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NAME: Campbell, Cathryn A.
REGISTATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LT
TELECOMMUNICATION INFORMATION:
TELEFRAM: (619) 535-9001
TELEFRAM: (619) 535-901
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08818514; Patent No. 5837838; GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 29; Conservative
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   (without alignments)
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              383533 seqs, 122816752 residues
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Listing first 45 summaries
                                                                                                                            OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                 US-09-721-543A-12
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length: 200000000
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Maximum Match 10
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Length 2634; Indels

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NAME: Campbell, Cathryn A.
REGISTRATHON NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 3209
TELECOMMUNICATION INFORMATION:
                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/818,514
FILING DATE: 14-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/818,514
FILING DATE: 14-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09115934A Patent No. 6130317 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPANE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ 1D NO: 2:
SEGUENCE CHARACTERISTICS:
LENGTH: 2634 base pairs
                                                                                                                                                                                                                                                                                        LENGTH: 2634 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 74.4
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California
COUNTRY: United States
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                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY:
US-09-115-934A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-115-934A-2
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Pred. No. 0.81;
0; Mismatches 10; Indels
GENERAL INCORATION:
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Xu, Qunli
TITLE OF INVENTION: BAX Inhibitor Proteins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reed, John C.
APPLICANT: Xu, Qunli
TITLE OF INVENTION: BAX Inhibitor Proteins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,934A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICAL
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARATERISTICS:
'FINGTH: 2634 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NS-09-115-934A-1/C
; Sequence 1, Application US/09115934A
; Patent No. 6130317
; GENERAL INFORMATION:
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TYPE: nucleic acid
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Best Local Similarity 74.4;
Matches 29; Conservative
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              US-08-818-514-2
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Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PatentIn Ralease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,934A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 2056 TCCACCCACACTTGAAGCCACAAAACTGCAGGGATTGGG 2018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: Callfornia
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APPLICANT: Xu, Qunl1
TITLE OF INVENTION: BAX Inhibitor Proteins
UNDMER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/CDCKET NUMBER: P-LJ 3209
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
SEQUENCE CHARACTERISTICS:
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Rajendra

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Kumar-Singh,
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           Length 2634;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,609
                                                10;
                                                                                                                                                                                                                                                                     APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Humar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
CORRESPONDENCE ADDRESS:
                                                                                                          Ouery Match 50.0%; Score 20; DB 2; Best Local Similarity 72.2%; Pred. No. 15; Matches 26; Conservative 0; Mismatches 1
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                                                                                     2 tegagecaceceataacecteaataetecagggattggg
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San Francisco
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           Score 23; DB 3 Pred. No. 0.81; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08735609
Patent No. 5994132
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                           Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
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Hauser, Michael A.
                                                                                                                                                                                                                 Sequence 9, Application US/08735609
Patent No. 5955360
           57.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3364 base pairs
           Ouery Match 57.5
Best Local Similarity 74.4
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Chambe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94104
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                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
Hartigan-O'Connor, Dennis J. INVENTION: IMPROVED ADENOVIRUS VECTORS
                                                                                                 ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Hauser, Michael A.
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENCYIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2326 AGCCTGCCCTCACCCTGGATCCACCAGGGACAGGG 2291
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STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20; DB 2
Pred. No. 15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAT: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        COUNTRY: United States Of America ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/735,609
FILING DATE: 23-Oct-1996
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLGGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States Of America
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Patent No. 6057158
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                        CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 50.0%;
Best Local Similarity 72.2%;
Matches 26; Conservative (
                                                                         CORRESPONDENCE ADDRESS:
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Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/245,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Hauser, Michael A.
APPLICANT: Winar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SOUTHNORS: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      2326 AGCCTGCCCTCACCCTGGATCCACCAGGGACAGGG 2291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: Callfornia
                                                                                                                                                                                                                                                                                               5 agccacccataaccctcaatactccagggattggg 40
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/735,609
APPLICATION NUMBER: -6B) FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: -0W-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
'PMCTH: 3364 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States Of America ZIP: 94104

    MOLECULE TYPE: other nucleic acid
    DESCRIPTION: /desc = "bNA"
US-09-244-752-9

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DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-245-497-9/c;
Sequence 9, Application US/09245497;
Patent No. 6083750;
GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
    LENGTH: 3364 base pairs
                                                                                                                                                                                                 Query Match
Best Local Similarity 72.2'
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 50.0
Best Local Similarity 72.2
Matches 26; Conservative
                     nucleic acid
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                            TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VETSION #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalitiano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Rumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2326 AGCCTGCCCCTCACCTGGATCCACCAGGGACAGGG 2291
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ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40.027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: California
COUNTRY: United States Of America
US/09/315,372
                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/735,609
FILING DATE:
                                                                                                                                                                                                    UM-02484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/244,75;
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/735,609
FILING DATE:
                                                                                                                    ATTORREY AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/POCKET NUMBER: UM-02
RELECOMMUNICATION INFORMATION:
TELEFONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3364 base pairs
TYRE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/09244752
Patent No. 6063622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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Sequence 10, Application US/09221236
Patent No. 6146841
GENERAL INFORMATION:
APPLICANT: AACLON. SUSAN
TITLE OF INVENTION SUSAN
FILE REFERENCE: MNI-050
CURRENT PELICATION NUMBER: US/09/221,236
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
EARLIER FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
                                TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR FILE REFERENCE: MIL-050
CURRENT APPLICATION NUMBER: US/09/221,527
CURRENT FILING DATE: 1998-12-28
EARLIER FILING DATE: 09/163,115
BARLIER FILING DATE:
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
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Petent No. 6153417
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-050
CURRENT APPLICATION NUMBER: US/09/221,416
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
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Pred. No. 29;
0; Mismatches
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Pred. No. 29;
0; Mismatches
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Best Local Similarity 67.5%;
Matches 27; Conservative
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Best Local Similarity 67.55
Matches 27; Conservative
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; LOCATION: (275)..(754)
US-09-221-527-10
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US-09-221-236-10
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  GENERAL INFORMATION:
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LENGTH: 1864
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LENGTH: 1864
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TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: MAI-050
CURRENT APPLICATION NUMBER: US/09/221,928
CURRENT APPLICATION NUMBER: 09/163,115
EARLIER FILING DATE: 1998-12-28
EARLIER FILING DATE: NUMBER: 09/163,115
SOFTHARE: PATCHIN NOVER: 2.0
SOFTHARE: PATCHIN VET. 2.0
                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-050
CURRENT APPLICATION NUMBER: US/09/221,235
CURRENT FILING DATE: 1998-12-28
EARLIER PAPLICATION NUMBER: 09/163,115
EARLIER FILING DATE:
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET. 2.0
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2326 AGCCTGCCCTCACCCTGGATCCACCAGGGACAGGG 2291
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Pred. No. 29;
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; Patent No. 6121030
; GENERAL INFORMATION:
                                                                                            ; Sequence 10, Application US/09221235; Patent No. 6043040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 10, Application US/09221527
; Patent No. 6146832
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Best Local Similarity 67.5%;
Matches 27; Conservative
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Best Local Similarity 67.59
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; LOCATION: (275)..(754)
US-09-221-928-10
                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (275)..(754)
US-09-221-235-10
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LENGTH: 1864
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US-09-221-527-10
                                                         RESULT 10
US-09-221-235-10
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Sequence 10, Application US/09221245
Sequence 10, Application US/09221245
Sequence 10, Application US/09221245
GENERAL INFORMATION:
APPLICANT: Acton, Susan
TITLE OF INFUNITON:
FILE REFERENCE: MN1-050
CURRENT TAPLICATION NUMBER: US/09/221,245
CURRENT APPLICATION NUMBER: US 09/163,115
EARLIER APPLICATION NUMBER: US 09/163,115
SEARLIER APPLICATION NUMBER: US 09/163,115
SEARLIER PLILNG DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
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48.0%; Score 19.2; DB 4; Length 1864;
Best Local Similarity 67.5%; Pred. No. 29;
Matches 27; Conservative 0; Mismatches 13; Indels 0;
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Best Local Similarity 67.5%; Pred. No. 29;
Matches 27; Conservative 0; Mismatches 13; Indels
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Job time: 6582 sec
EARLIER FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 10
LENGTH: 1864
                                                                                                               TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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ORGANISM: Homo sapiens
                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (275)..(754)
US-09-221-416-10
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; LOCATION: (275)..(754)
US-09-221-245-10
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                                    bone marrow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ligand; human cytomegalovirus; HCMV infection; herpetic ulcer; pneumonia; gastroenteritis; chorioretinitis; antiviral agent;
                                                     Probe
                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
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AAI96641
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ABL32625
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AAK31288
AAI37184
AAX37371
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AAS16876
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AAS81354
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Synthetic.
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 WO200138341-A1.
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AAD10599;
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 RESULT
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Bax inhibitor BI-1
Lung cancer associ
Human foetal liver
Probe #16250 for g
Human brain expres
                                                                                                                    4, 2002, 15:57:52; Search time 521.5 Seconds
(without alignments)
131.690 Million cell updates/sec
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Probe #20651 used
Human foetal liver
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SIDSI / Goddata/geneseq/geneseqn-embl_/Nal998 .DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS1/gcgdata/geneseq/genesegn-emb1/NA2002.DAT:*
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              version 4.5
- 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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AAV59067
AAF18054
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ABA37784
AAK20013
AAK46055
AAI51965
                                                                                    nucleic search, using sw model
                                                                                                                                                                                                                                                                                   Gapop 10.0 , Gapext 1.0
                GenCore
Copyright (c) 1993
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Maximum DB seq length: 200000000
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herpesvirus infections e.g. primary or chronic infections with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This cDNA clone codes for an inhibitor protein, termed BI-1 (see AAW73136), of the pro-apoptotic protein Bax. Nucleic acids encoding BI-1 and BI-2 (see AAV59068) were identified by suppression of bax-induced death of yeast cells transformed to express human Bax. A human HepG2 cDNA library was used for library screening. The invention provides vectors, optionally expression or viral vectors, containing BI nucleic acids, and host cells containing these vectors. The nucleic acids encoding BI-1/BI-2 can be used to
                                                                                          herpesvirus, particularly human cytomegalovirus (HCMV) to decrease or block HCMV infection in target cells. These ligands are used as anti-viral agents for the treatment of herpesvirus infections (e.g. lesions and herpetic ulcers) and particularly HCMV associated primary or chronic infections such as pneumonia, gastroenteritis and chorioretinitis. The present sequence is DNA ligand which bind to HCMV to decrease or block HCMV infection in target cells.
                                                                                                                                                                                                                                                                                                          ö
                                                                             The invention relates to polynucleotide ligands which bind to
                                                                                                                                                                                                                                                                            Length 40;
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                                                                                                                                                                                                                                                                                                                                         1 ctcgagccaccccataaccctcaatactccaggattggg 40
                                                                                                                                                                                                                                                                                                                                                                     1 ctcgagccaccccataaccctcaatactccagggattggg 40
                                                                                                                                                                                                                                                                       100.0%; Score 40; DB 22;
100.0%; Pred. No. 1.1e-07;
11ve 0; Mismatches 0;
                                                                                                                                                                                                                      Sequence 40 BP; 10 A; 15 C; 8 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bax inhibitor; BI-1; human; apoptosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
73..786
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 61-63; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                               Page 6; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV59067 standard; cDNA; 2634
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                                                                                                                                                                                                                                                                                                         40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bax inhibitor BI-1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-531519/45.
P-PSDB; AAW73136.
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Matches 40; Conserv
                cytomegalovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                               Claim 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences. The lung cancer associated chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAFI8425 - AAFI8433 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; and immunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antlinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the
                                                                                                                                                                                                              Gaps
increase expression of these proteins in cells, or antisense molecules prepared from them used to decrease expression. In these ways, cellular apoptotic activity may be modulated (claimed). The nucleic acids and complementary sequences are also useful as probes to detect BI-encoding nucleic acid molecules in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; lung cancer associated protein; neuroprotective; cytostatic;
                                                                                                                                                                                                              ö
                                                                                                                                                                     Length 2634;
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                                                                                                                                                                                                              Indels
                                                                                                                Sequence 2634 BP; 632 A; 626 C; 597 G; 779 T; 0 other;
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                                                                                                                                                         57.5%; Sco...
74.4%; Pred. No. 4...
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                AAF18054 standard; DNA; 2922 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAR-2000; 2000WO-US05918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0124270.
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                                                                                                                                                                   Query Match
Best Local Similarity
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Probe #16250 for gene expression analysis in human heart cell sample.
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   2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-023366.
2000US-0234687.
                                                                                           ABA37784 standard; DNA; 121
                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00666
                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                         WO200157274-A2.
                                                                                                                                                                                                                                                                              Homo sapiens.
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04-OCT-2000;
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21-SEP-2000;
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30-JUN-2000;
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ABA37784/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Wote: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver \dot{}
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                                                                                                      Score 23; DB 21; Length 2922;
Pred. No. 4.2;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; SEQ ID NO 19974; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                    Human foetal liver single exon nucleic acid probe #19974.
                                                          Sequence 2922 BP; 712 A; 686 C; 654 G; 863 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
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Pred. No. 14;
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26-MAX-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                        57.5%;
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76.5%;
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2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                     29; Conservative
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Best Local Similarity 76.5
Matches 26; Conservative
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                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2000;
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                                 sednences
                                                                                                      Query Match
Best Local Si
Matches 299
                                                                                                                                                                                                                                                                                                        ABA71669;
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                                                                                                                                                                                                                                                                                                                                                                                                                           measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosting, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes for
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Pred. No. 14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 ccaccccataaccctcaatactccaggga:tggg 40
                                                                                                                                                                                                                                                                                                                                Claim 4; SEQ ID No 16250; 530pp; Erglish.
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                                                              (MOLE-) MOLECULAR DYNAMICS INC
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Best Local Similarity 76.5%;
Matches 26; Conservative (
2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              congenital heart disease.
                                                                                                                          Hanzel DK,
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AAK20013/c
ID AAK200
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0; Mismatches

7 ccaccccataaccctcaatactccagggattggg 40

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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO: 20612; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 121 BP; 46 A; 20 C; 28 G; 27 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 ccaccccatuaccctcaatactccagggattggg 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.0%; Score 21.2; 76.5%; Pred. No. 14;
                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                        26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-060B40B.
03-AUG-2000; 2000US-053256.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                        Chen W,
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the probes of the invention.
                                                             2:001WO-US00668
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ID AAI51965 standard; DNA; 121
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2000GB-0024263.
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                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genetic disorder; ss.
                                                                                                                                                                                                                                                                                     WPI; 2001-488900/53.
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WO200157276-A2.
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                                                           30-JAN-2001;
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21-SEP-2000;
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04-OCT-2000;
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                               09-AUG-2001
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                                                                                                                                                                                                                                                        Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI51965;
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Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schlzophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in human brains -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                      Human; brain expressed exon; gene expression analysis; probe; microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          marrow expressed exon; gene expression analysis; probe; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO: 20004; 650pp + Sequence Listing; English.
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                                                                         Human brain expressed single exon probe SEQ ID NO: 20004.
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llarity 76.5%; Pred. No. 14;
Conservative 0; Mismatches
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2000US-0207456.
2000US-0608408.
2000US-0632366.
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2000US-0236359.
2000GB-0024263.
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                                         05-NOV-2001 (first entry)
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                                                                                                                                        epilepsy; cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-483446/52.
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les 26; Conserv
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27-SEP-2000;
04-OCT-2000;
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30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                  04-FEB-2000;
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           AAK20013;
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Matches
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Length 121; Indels

DB 22; .;

DR; Rank

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to measure gene expression in human placenta sample.
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                                                                                                                                                       The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                   genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
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                                                                                                                                                                                                                                                                                         Length 121;
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                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human foetal liver single exon nucleic acid probe #7450.
                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                              Sequence 121 BP; 46 A; 20 C; 28 G; 27 T; 0 other;
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                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                      Score 21.2; DE Pred. No. 14; 0; Mismatches
                                                                                                    analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                 7 ccaccccataaccctcaatactccagggattggg 40
                                                                                                                             Claim 25; SEQ ID No 20651; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                DR;
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MOLECULAR DYNAMICS INC.
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                             Chen W,
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2000US-0207456.
2000US-0608408.
2000US-0632366.
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31-SEP-2000; 2000US-052356.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0235359.
04-OCT-2000; 2000GB-0024263.
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ilarity 76.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                               Hanzel DK,
                                                        WPI; 2001-488897/53
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es 26; Conser
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Best Local (
                             Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single exon nucleic acid probes for analyzing gene expression in human hearts .
probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe #6388 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention relates to single exon nucleic acid probes
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                                                                                                                                                                                                                   Length 473;
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cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                     Indels
                                                                                                                                 Sequence 473 BP; 144 A; 91 C; 95 G; 143 T; 0 other;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                      7 ccaccccataaccctcaatactccagggattggg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            congenital heart disease; ss.
                                                                                                                                                                                                              53.0%;
76.5%;
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2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                              Query Match 53.0
Best Local Similarity 76.5
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488899/53
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA27922;
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphona, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe #7579 used to measure gene expression in human placenta sample.
                                                                                                                              Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-darived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO: 7652; 658pp + Sequence Listing; English.
                                                                                               Human bone marrow expressed single exon probe SEQ ID NO: 7652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 473 BP; 144 A; 91 C; 95 G; 143 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 18;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 ccaccccataaccctcaatactccagggattggg 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR;
AAK33095 standard; DNA; 473 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                                                                                                                                                         2000US-0180312.
2000US-0207456.
2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-023687.
7-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00668
                                                               (first entry)
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Best Local Similarity 76.5
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488900/53.
                                                                                                                                                                                                           WO200157276-A2
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                                                                                                                                                                              Homo sapiens.
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                                                              06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in human brains -
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                        Human; brain expressed exon; gene expression analysis; probe; microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
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               Length 473;
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                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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             22;
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               В
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           Score 21.2; Di
Pred. No. 18;
0; Mismatches
                                                                                            40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 21.2;
Pred. No. 18;
                                                                          7 ccaccccataaccctcaatactccagggattggg
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                                                                                                                                                                                            ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-UJN-2000; 2000US-0608408.
03-AUG-2000; 2000US-023366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.0%;
76.5%;
             53.0%;
76.5%;
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ID AAK07330 standard; DNA; 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                                                        (first entry)
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                                             Conservative
                                                                                                                                                                                                                                                                                                                                                       epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483446/52
           Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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Gaps

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Length 473; Indels

22; 8

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RESULT 12 AAK33095/c

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proteins they encode. The products of the invention are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 101 polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and fetal neurodegenerative disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, Alzehamer's and cognitive disorders; pulmonary disorders, transplant rejection, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, digestive/endocrine disorders, infections and AIDS. The human secreted proteins of the invention are represented in AAX07852-v07993 and the encoding nucleic acids are
                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel isolated human genes and the secreted
                                                                                                                                                                                                                                                                                                                                            New isolated human genes and the secreted polypeptides they encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 12758.
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                                                                                                                                                                                            Jan DR, Endress GA, Feng P, Ferrie AM; Greene JM, Janat F, Lafleur DW, Ni J; Den SM, Shi Y, Young P, Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 837 BP; 171 A; 249 C; 187 G; 228 T; 2 other;
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Pred. No. 29;
0; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                  Claim la; Page 264; 368pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL06092
ID ABL06092 standard; cDNA; 3896
97US-0060838.
97US-0060839.
97US-0060843.
97US-0060862.
                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
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Best Local Similarity 70.0%;
Matches 28; Conservative
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                                                                                                          97US-0060874
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                                                                                                                                                                                                       Florence KA, Greeue
                                                                                                                                                                                            Duan DR,
                                                                                                                                                                                                                                                                            WPI; 1999-264022/22
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                                                                                                          02-OCT-1997;
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                                            02-OCT-1997;
02-OCT-1997;
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                                                                                                                                                                                              Carter KC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 473 BP; 144 A; 91 C; 95 G; 143 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                analyzing gene expression in human placenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID No 7579; 654pp; English.
                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0623466.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
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97US-0060836.
97US-0060837.
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                                                                30-JAN-2001; 2001WO-US00663
                                                                                                          2000US-0180312
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                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 26; Conserv
                                                                                                        04-FEB-2000;
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02-OCT-1997;
02-OCT-1997;
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                   09-AUG-2001
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AAX37525/c

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Length 837; Indels

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PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

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PA (PEKE ) PE CORP NY.

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PI (PEKE ) PE CORP NY.

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WHI; 2001-655860/75.

DR P-PSDB; ABB61989.

XX

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell pr interactions -

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is cuseful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapoutics and pharmaceutical drugs. The invention CC discloses genomic DNA sequences (ABL61076-ABL30511), expressed DNA sequences (ABL01840-ABL305115) and the encoded proteins (ABS57737-ABB72072).

CT he sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO XX

Squence 3896 BP; 1147 A; 931 C; 883 G; 935 T; 0 other;
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Search completed: June 4, 2002, 17:56:12 Job time: 7100 sec sapi

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AC090230 Homo sapi
AC087535 Homo sapi
AP001592 Homo sapi
AC010367 Homo sapi
297198 Human DNA s
G22123 human STS W
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                                                                                                                                                                                                                                                                                     AL035663 Human DNA
Continuation (5 of
AL513483 Homo sapi
AL662983 Oryza sat
AL445199 Homo sapi
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Homo sapiens signet-ring cell carcinoma cell_line:KATO III cDNA to
mRNA, clone_lib:KAT clone:KATO9742.
                                                                                                                  Homo sapi
Human DNA
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Sequence
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Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.
Direct Submission
Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio
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Eukaryota; Metazoa; Chordatz; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watanabe, K., Kumagai, A., Itakura, S., Yamazaki, M., Tashiro, H., Ota, T., Suzuki, Y., Cobayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Namurus, Y., Isogai, T. and Sugano, S.
NEDO human cDNA sequencing project
Unpublished (2000)
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AL445228
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AC010367
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Homo sapiens cDNA: FLJ22952 fis, clone KAT09742.
AK026605
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                                                        4, 2002, 15:55:32 ; Search time 2137.99 Seconds (without alignments) 391.518 Million cell updates/sec
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                         1797656 segs, 10463268293 residues
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Maximum Match 100%
Listing first 45 summaries
                                        OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Score

Result

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Strausberg, R.
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Best Local
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Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mall:cdnal@ims.u-tokyo.ac.jp, Tel.81.3-5449-5286, Fax:81-3-5449-5246)
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; CDNA library construction, S. - & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, Divinersity of Tokyo (Partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-JAN-1994) L. Walter, Abteilung Immungenetik der Universitaet Goettingen, Gosslerstr 12d, 37073 Goettingen, FRG (bases 1 to 2600) Walter, L., Marynen, P., Szpirer, J., Levan, G. and Gunther, E. Identification of a novel conserved human gene, TEGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                           /cell_type="signet-ring cell carcinoma"
/clone="KAT09742"
/clone="KAT09742"
/note="cloning vector pME185FL3"
369 c 358 g 485 t
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Pred. No. 32;
0; Mismatches
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/organism="Homo sapiens"
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/organism="Homo sapiens"
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X75861
X75861.1 GI:456258
FEGT gene.
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Best Local Similarity 74.4
Matches 29; Conservative
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 3 Row: k Column: 7 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 2645728.
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//db_xref="GI:13111819"
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AVHWTHETOAGLLSALGSILLMHUMATPHSHETBCRKIGLLAGFRIGVGPA
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NVFFGSIWLFQANLYVGLVVMCGFVLFDTQLLIEKABHGDQDYIWHCIDLFLDSTTY
NVFFGSIWPFQANLYVGLVVMCGFVLVDTQLIIEKAEHGDQDYIWHCIDLFLDFITVF
RKLMMILAMNEKDKKKKKKK"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2609)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission Submitted (16 NOV-2000) National Institutes of Health, Mammalian Submitted (16 NOV-2000) National Institutes Office, National Cancer Gene Collection (MCC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2609 bp mRNA linear PRI 12-JUI
Homo sapiens, testis enhanced gene transcript, clone MGC:5230
IMAGE:2300280, mRNA, complete cds.
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Web Site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu
villalon; D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., G
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
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Pred. No. 31;
0; Mismatches 10; Indels
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74.48;
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AC019168 197189 bp DNA linear HTG 07-JUL-2000 HOMO sapiens chromosome 12 clone RP11-161E16, WORKING DRAFT SEQUENCE, 24 unordered pieces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 31;
0; Mismatches 10; Indels
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Pred. No. 31;
0; Mismatches
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1 (bases 1 to 2634)
Reed.J.C. and Xu,O.
Bax inhibitor proteins
Patent: US 6130317-A 2 10-0:T-2000;
Location/Qualifiers
                                                                                                                                                                                                                                    1 (bases 1 to 2634)
Reed, J.C. and Xu,0.
Bax inhibitor proteins
Patent: US 6130317-A 1 10-0CT-2000;
Location/Qualifiers
1. .2634
                                                                AR112791 2634 bp
Sequence 1 from patent US 6130317,
AR112791 GI:14092691
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Sequence 2 from patent US 6.130317
AR112792
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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626 c 597 g
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Best Local Similarity 74.4%;
Matches 29; Conservative (
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Best Local Similarity 74.4%;
Matches 29; Conservative
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                                                                                  DEFINITION
ACCESSION
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                        RESULT 6
AR112791/c
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TITLE
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Pred. No. 31;
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Pred. No. 31;
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Pred. No. 31;
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Sequence 1 from patent US 5837838.
AR058920 GI:5984497
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Sequence 2 from patent US 5837838.
AR058921
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Unclassified.
1 (bases 1 to 2634)
Red J.C. and Xu.Q.
Bax inhibitor proteins
Patent: US 5837838-A 2 17-NOV-:
Location/Qualifiers
RKLMMILAMNEKDKKKEKK"
1 625 c 602 g
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597 c 626 g
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626 c 597 g
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                                                                                                         57.5%;
74.4%;
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Best Local Similarity 74.4%;
Matches 29; Conservative
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Best Local Similarity 74.4%;
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COMMENT

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130 107954: contig of 14825 bp in length 1955 108054: gap of unknown length 1055 121842: contig of 13788 bp in length 121842: gap of unknown length 131362: contig of 15420 bp in length 363 137462: gap of unknown length 155524: contig of 18062 bp in length 525 155624: gap of unknown length 625 173416: contig of 17792 bp in length 417 173516: gap of unknown length 417 173516: gap of unknown length 617 197189: contig of 23673 bp in length 10081197189: contig of 23673 bp in length 10081107792 bp in length 617 197189: contig of 23673 bp in length 10081107792 bp in lengt
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                        of 15466 bp in length
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18692. 58168
note="assembly_name:Contig17"
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/note="assembly_name:Contigl8"
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//octe="assembly_name:Contig20"
93130. 107954
//octe="assembly_name:Contig21
clone_end:SP6
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21943. 137362
note="assembly_name:Contig23"
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/note="assembly_name:Contig24"
155625. .173416
/note="assembly_name:Contig25"
173517. .197189
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note="assembly_name:Contig3"
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/note="assembly_name:Contig4"
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note="assembly_name:Contig8"
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note="assembly_name:Contig9"
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note="assembly_name:Contig5"
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note="assembly_name:Contig6"
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note="assembly_name:Contig7"

    .197189
    /organism="Homo sapiens"
/db_xref="taxon:9606"
    /chromosome="12"

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gap of
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108055. .121842
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ORIGIN
                                                                                                                                                                                                                                                              FEATURES
                                                                                                        Direct Submission
Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mn 63108, USA
On Mar 13, 2000 this sequence version replaced 91:7021812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                     Quality coverage: 3.69 in Q20 bases; agarose-fp Quality coverage: 3.65 in Q20 bases; sum-of-contigs
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Manmalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

Mary D.M., Adams.C., Adio-Oduola, A. Ali-Osman, F.R., Allen, C., Abarboroks, S.L., Amaratunge, H.C., Arej.R., Apter, M., Banks, T., Barbaria, J., Bandan, C., Birkey, M., Brown, E., Brown, M., Baryant, N., Barbay, T., Barbay, C., Barter, M., Cavazos, S.R., Charcko, J., Chavez, D., Char, C., Coyle, M.D., Dathorne, S.R., David, R., Delaney, K.R., Delan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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115867 bp DNA linear HTG 31-,
Homo sapiens chromosome 12q clone RP11-382G3, WORKING DRAFT
ACORANA.
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74.4%;
                             Local Similarity 74.4 tes 29; Conservative
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On Jan 31, 2002
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Sequencing vector: Plasmid; M7789
Sequencing vector: Plasmid; M7789
Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 2% of reads
Chemistry: Dye-terminator B1g Dye: 98% of reads
Assembly program: Phrap; version 0.990329First call to
findPhraphist
Consensus quality: 223543 bases at least Q40
Consensus quality: 227846 bases at least Q30
Consensus quality: 229658 bases at least Q30
Estimated insert size: 217093; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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NOTE: This is a "working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available, and the accession number will be preserved.
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contig of 4228 bp in length
gap of unknown length
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                          Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                  Center project name: HCHJ
Center clone name: RP11-382G3
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Best Local Similarity 74.44
Matches 29; Conservative
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

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Manmalla Eucheria; Pilmates; Catarrhini; Hominidae; Homo.

Manmalla; Eucheria; Pilmates; Catarrhini; Hominidae; Homo.

Reses; 1 to 225819

Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-Osman, F. R., Allen, C., Alabrooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Banka, T., Babrooks, S. L., Barton, J. Blancon, D. Barton, E., Brown, M., Baryan, D. Barton, D., Bouch, P., Burch, P., Burch, P., Burch, E., Burch, E., Brieden, G., Chen, R., Chen, C., Coyle, M. D., Dathorne, S. R., David, N. C., Coyle, M. D., Dathorne, S. R., David, R., Datalany, K. R., Dabland, C. D., Cox, C., Coyle, M. D., Dathorne, S. R., David, R., Delandy, C., Draper, H., Dugan-Rocha, S., Durbin, K. J., Davis, C., Davy, Carroll, L., Dederich, D. A., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gartal, A., Garta, A., Garrer, T., Garza, N., Gall, R., Garrell, A., Garcia, A., Garrer, T., Garza, N., Gall, R., Garrell, J. H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K., Harrandez, O., Hoddson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, O., Hoddson, A., Hogues, M., Holloway, C., Hollins, B., Harrisson, B., Jacobson, B., Jacobson, B., Jacobson, B., Jacobson, B., Jacobson, B., Jackson, L. E., Jacobson, B., Jacobson, B., Jacobson, B., Jacobson, B., Jacobson, B., Martinez, E., Martisson, B., Jacobson, B., Jacobson, B., Jacobson, B., Martin, W., Leal, B., Martin, C., Lat, J., Lil, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality coverage: 0x in Q20 bases; agarose-\tilde{f}p estimation Quality coverage: 4.9x in Q20 bases; sum-of-contigs estimation
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 259159 bases at least Q40
Consensus quality: 268975 bases at least Q30
Consensus quality: 275062 bases at least Q30
Estimated insert size: 250108; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
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Assembly program: Phrap; version 0.990329First call to
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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Direct Submission
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Homo sapiens chromosome 18 clone RP11-873L22 map 18q21, WORKING DRAFT SEQUENCE, 18 unordered pieces.
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                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
NOTE: This sequence may represent more than one clone. NOTE: This is a "working draft' sequence. It currently consists of 20 contings. The true order of the pieces is not known and their order in this sequence record is
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contig of 10915 bp in length
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Best Local Similarity 74.4'
Matches 29; Conservative
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TITLE

COMMENT

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82758 82857: gap of 100 bp 82858 9554: contig of 12687 bp in length 82858 9554: contig of 12687 bp in length 95545 9554: contig of 13948 bp in length 109593 109592: gap of 100 bp 100 bp 120268 120267: gap of 100 bp 120268 120255: contig of 100 bp 120268 120255: contig of 100 bp 120268 120255: gap of 100 bp 120268 120255: gap of 100 bp 120268 120255: gap of 100 bp 120268 120255: contig of 6988 bp in length 120268 120255: contig of 7648 bp in length 137004 137103: gap of 100 bp 100 bp 144376: contig of 7273 bp in length 144376: gap of 100 bp 100 bp 150060 150599: gap of 100 bp 100 bp 150060 150599: gap of 100 bp 160522: contig of 5137 bp in length 150060 150599: gap of 100 bp 160522: gap of 100 bp 160523 160522: gap of 100 bp 160524 163363: gap of 100 bp 160524 163363: gap of 100 bp 165264 165194: contig of 2410 bp in length 165195 165294: gap of 100 bp 165295 165294: contig of 2410 bp in length 165195 165294: gap of 100 bp 165295 167704: contig of 2410 bp in length 165195 165294: gap of 100 bp 165295 167704: contig of 2410 bp in length 165195 165294: contig of 26
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82757: contig of 15587 bp in length
82857: gap of 100 bp
     24923: contig of 24923 bp in length
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67070: contig of 19966 bp in length
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/clone="RP11-873L22"
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                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases I to 171185)
Hattori, M., Ishi, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Homo sapiens 171,185 genomic DNA of 18q21
Published Only in DataBase (2000) In press 2 (bases 1 to 171185)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Submission
Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
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                                                                                                                                                                                                                                                                                                                                                                                                                                  and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hpg.gsc.riken.go.jp/, Tel:81-42-778-9923,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center clone name: RP11-873L22
Sequencing vector: PCR products; 100% of reads
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 156977 bases at least Q40
Consensus quality: 164110 bases at least Q30
Consensus quality: 167421 bases at least Q30
Insert size: 169485; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 4.80x in Q20 bases; sum-of-contigs
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Contact: hattori@gsc.riken.go.jp
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Homo sapiens DNA, clone:RP11-873L22.
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                                                                                                        Homo sapiens
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ACCESSION
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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* NOTE: This is a 'working draft' sequence. It currentl
* consists of 32 contigs. The true order of the pieces
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81254 81353: gap of 100 bp
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APROUS69
APROUS69
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HTG; HTGS DIARREN
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Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 177,097 genomic DNa of 18921
Published Only in Database (2000) In press
1 to 177097)
Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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a 32086 c 33289 g 52078 t
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Homo sapiens DNA, clone:RP11-859C21
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6207 7415 6105 5644 6634 6634 5300 5148 4255 3683 3667 3885

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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 179726)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

(Inpublished

I (bases 1 to 179726)

Birren, B. Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barna, J., Barna, N., Beckely, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, N., Cooke, P., Dearellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Raratas, A., Lehoczky, J., Heu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGrernan, K., McGanald, P., Maylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavilin, J., Molla, M., Morris, W., Morrey, J., Mychaleckyj, J., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavilin, B., Beterson, K., Pollaraw, V., Riley, R., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vew, J., Wu, X., Wuw, X., Wu, X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC007052 179726 bp DNA linear PRI 23-MAR-1999
Homo sapiens chromosome 18, clone hRPK.411_H_24, complete sequence.
AC007052
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                                                                                Score 22.8;
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    in length
154046: contig of 3893 bp
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1 ctcgagccacccataaccctcaatactccaggg 34

Ouery Match 57.0%; Score 22.8; DB 9; Length 179726; Best Local Similarity 79.4%; Pred. No. 33; Matches 27; Conservative 0; Mismatches 7; Indels 0;

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Gaps

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ACCESSION VERSION KEYWORDS

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soon as it is available and the accession number will
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Pred. No. 33;
0; Mismatches 7; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68999 69098: gap of 100 bp
69099 103010: contig of 33912 bp in length
103011 103110: gap of 100 bp
103111 182411: contig of 79301 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p of 100 bp
contig of 20182 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                    25231 25330; gap of 1391 bp in length 25331 35330; gap of 100 bp 25331 32077; contig of 6747 bp in length 32078 32177; gap of 100 bp 32178 48716; con+in of 100 bp
                                                                                                                                                                       100 bp
f 2395 bp in length
100 bp
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                                                                                                                                                                                                                                                                                                                                                                   p of 100 bp contig of 4385 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                  p of 100 bp contig of 7391 bp in length
                                                                                                                             of 100 bp contig of 1116 bp in length
                                                                                                                                                                                                                                                  1989 bp in length
                                                                             of 100 bp
contig of 884 bp in length
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/note="assembly_fragment"
35140 c 35375 g 54140 t
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13355 17739; conti
17740 17839; gap of
17840 25230; conti
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68998: cont
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/map="18"
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69099 103010: cont
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79.4%;
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7688 9739:
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1888 3003:
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Best Local Similarity 79.43
Matches 27; Conservative
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48817 6899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
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S Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Canarata, J., Campoplano, A., Chopel, Y., Colangelo, M., Collins, S., Collymorre, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Greellano, K., Dewar, K., Diaz, J.S., Collymorre, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, M., Jones, C., Karatas, A., LaRoque, K., Hulme, W., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRoque, K., Hulme, W., Illev, I., Johnson, R., Marquis, N., Matthews, C., McCarthy, M., McEwan, C., McKernan, K., Mrphy, T., Maylor, J., Mguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Riley, R., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Royn, Santos, R., Schuer, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Vallson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Nabmitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar IS, 2001, this sequence version replaced g1:12958044.

All repeats were identified using RepeatMasker: html

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                              ACO90408 182411 bp DNA linear HTG 09-MAY-2001
Homo sapiens chromosome 18 clone RP11-859C21 map 18, WORKING DRAFT
SEQUENCE, 14 unordered pieces.
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: 112718

Center clone name: 859_C_21

Center clone name: 859_C_21

Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 177348 bases at least Q30
Consensus quality: 179869 bases at least Q30
Consensus quality: 180657 bases at least Q30
Insert size: 181111; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality coverage: 6.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 182411)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Unpublished
                                                                                                                                                                                                                                        AC090408.2 GI:13357356
HTG; HTGS_PHASE1; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
Db 78718 CTCTAGCCTCCCCATGCCCCTCATTCTCCAGTG 78685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 182411)
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                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                               RESULT 14
AC090408/c
                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                 ORGANISM
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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
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TITLE JOURNAL

COMMENT

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Gaps

.38 of consensus"

8. .1231 of consensus*

.2611 of consensus"

.2272 of consensus"

.189 of consensus"

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/note="L1PB3 repeat: matches 5916, .6147 of consensus"
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1.2615. .12650
1.3016. .12650
1.3016. .14099
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29868. 30157
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16084. 16364
/note="AluJo repeat: matches 1.
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20737. .20812
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                                                                    repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eukharia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 188357)

1 Laird,G.

Direct Submission

Louiste Catarrhini; Hominidae; Homo.

2 Laird,G.

Direct Submission

Louiste City Compared (19-Jul-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jun 21, 2000 this sequence version replaced gi:8346239.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone ande. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw.; SWISSROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGPChr9
RPI1-401F12 is from the library RPCI-11.2 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                 188357 bp DNA linear PRI 24-JUL-2000 Human DNA sequence from clone RP11-401F12 on chromosome 9. Contains ALI59996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is the entire insert of clone RPI1-401F12 The true left end of clone RPI1-806G24 is at 167549 in this sequence. The true right end of clone RPI1-395D3 is at 5200 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .7077 of consensus"
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/note="2 copies 32 mer 96% conserved"
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/note="match: GSS: Em:AQ606829"
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note="match: GSS: Em:AQ823967"
1. .188357
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="RP11-401F12"
/clone_lib="RPCI-11.2"
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note="L1MC4 repeat:
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Query Match 57.0%; Score 22.8; DB 9; Length 188357; Best Local Similarity 79.4%; Pred. No. 33; Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps

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